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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	AKOO9815 LOCUS DEFINITION ACCESSION VERSION		41 42 44		33 3 4 G				20 21 22	16 17 18	13 14 15	10 11 12	987	4 N C	س دی ب	Result No.
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ciurognathi; Muridae; Murinae; Mus. A cloning	male tongue cDN mouse cDNA libr	HTC 08-FEB-2001 DNA, RIKEN full-length enriched insert sequence.	BG240463 OV1_30_D0	H36370 14892 Lambd H36370 14892 Lambd BE419958 WWS019.E6 BE520887 M15E5TTM	BF272517 GA_EB001 BF272517 GA_EB001 BE614098 601503838 AZ530400 ENTCN11TF	AW983497 HVSMEg001 AU061011 AU061011 AZ541451 ENTFK21F ATIONANA ATIONANA	N3/134 18469 Lambd BE196055 HVSMEh009 BE800662 Sq96e01.y BE196057 HVSMEh009	BG167785 602339921 AW004473 701931727 BE636603 rockefell	AA880470 vx40102.r BG366889 HVSMEi000 N65726 20766 Lambd AW397653 sgA2ff2 v	AU136141 AU136141 AU139463 AU139463 T23385 5c09b11 mem	BE414598 SCU011.E0 BF58594 FM1_23_C0 D48464 RICS14669A	AI79537 WHEUSU3_A AI795537 605011A01 AL043330 DKFZP4340 AI9937R5 701514536	AW05399 68/002G09 BE402623 CSB009H05 BG551002 Sad31h09.	AW244197 687050F06 AW244197 687050F06 AV442128 AV442128	BE193020 HYSMEHUUB BF065047 HY_CEb002 AW596011 s196g03.y	K009815 E602527	Description
	source	FEATURES		COMMENT		JOURNAL	ጥ ተጥ . ຄ			JOURNAL REFERENCE AUTHORS	AUTHORS	JOURNAL MEDLINE	TITLE		AUTHORS	JOURNAL	JOURNAL REFERENCE AUTHORS TITLE
/clone="2310045H19" /sex="male" /tissue_type="tongue" /clone_lib="RIKEN full /dev_stage="adult"	1. 2738 /organism="Mus musculu /strain="C57BL/6J" /db_xref="McD:MGI:1907 /db_xref="MGD:MGI:1907		Genomic Sciences Center and Gen Division of Experimental Animal prepare mouse tissues. First st [5 GAGAGAGAGAGGATCCAAGAGCTCTT prepared by using trehalose the and subsequently enriched for through one round of normalizat	Please visit our web site (http further details. cDNA library was prepared and s Encyclopedia Project of Genome	KINEW YOKONAMA INSTITUTE; 1-7-3 KANAGAWA 230-0045, Japan (E-mai URL:http://genome.gsc.riken.go Fax:81-45-503-9216)	Submitted (10-701-2000) Yoshihi Physical and Chemical Research Exploration Research Group, RII	,Y., Suzuki,H., (,T., Tejima,Y., , ,T., Tejima,Y., , , , , , , , , , , , , , , , , , ,	NOJ.Ma.I., KOHIO, H., KOUQA, M., Miyazaki, A., Nishi, K., Nomura, J Okido, T., Owa, C., Saito, H., Sa Sasaki, D., Shibata, K., Shibata	Arakawa, T., Carninci, P., Fukud Hanagaki, T., Hara, A., Hayatsu, I Imotani, K., Ishii, Y., Itoh, M.,	Nature 409, 685-690 (2001) 5 (bases 1 to 2738) Adachi,J., Aizawa,K., Akahira.	4 (SILES) The RIKEN Genome Exploration ReFANTOM Consortium.	sequencing pipeline with 384 m Genome Res. 10 (11), 1757-1771 20530913	Watahiki,M., Yoneda,Y., Ishika Matsuura,S., Okazaki,Y., Muram RIKEN integrated sequence anal	Kikuchi, N., Ishii, Y., Nakamura Harada, A., Yamamoto, R., Matsum Kashiwaqi, K., Fujiwake, S., Ino	<pre>3 (sites) Shibata,K., Itoh,M., Aizawa,K. Konno,H., Akivama,J., Nishi,K.</pre>	<pre>prepare full-length cDNA libra Genome Res. 10 (10), 1617-1630 20499374</pre>	Methods Enzymol. 303, 19-44 (1 2 (sites) Carninci, P., Shibata, Y., Hayat Itoh, M., Konno, H., Okazaki, Y., Normalization and subtraction

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ira,S., Akimura,T., Aono,H., Arai,A., ukuda,S., Fukunishi,Y., Furuno,M., tsu,N., Hiramoto,K., Hiraoka,T., Hori,F.,M., Izawa,M., Kato,H., Kawai,J., M., Koya,S., Kurihara,C., Matsuyama,T., ura,K., Numazaki,R., Ohno,M., Okazaki,Y., Saito,R., Sakai,C., Sakai,K., Sano,H., bata,Y., Shinagawa,A., Shiraki,T., mi,M., Tagawa,A., Takahashi,F., T., Yamamura,T., Yasunishi,A., ramatsu,M. and Hayashizaki,Y.
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iti,K., Kitsunal,T., Tashiro,H., Itoh,M.,
imura,S., Hazama,M., Nishine,T.,
itsumoto,H., Sakaguchi,S., Ikegami,T.,
Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
hikawa,T., Ozawa,K., Tanaka,T.,
uramatsu,M., Inoue,Y. and Hayashizaki,Y.
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T., Muramatsu,M. and Hayashizaki,Y.
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                                                                                           651 GGAAAAATAGCTTCTTACAAACATTTTACCAGCAATGTACTACCAAGAATCAAAGACCTT 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gacatagatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagtac 521
                                                                                                                                                                                                                                                                                                                                                                                                                                      aaa---gattctattcctgcttggatcaagttctcagttcaagcaccaggtgaactccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtcatgactcagaatgagtgtggtgtctgggagatctttttgccgaataatgcagatggt 758
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                                                                                                                                                                                              CCTAAGAAACCAAGAAGCCTAAGAATTTATGAATCTCATGTGGGAATTTCTTCCCACGAA 650
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/Translation="MARPAPARAETGPDARLEAALADVPELARLLEIDPYLKPFAAD
FQRRYKKFSQYLHDIGENEGGIDKFSRGYESFGIHROSDGGITCKEWARPGAEGVFLIG
FPORNYENENUNVYDWIHMAPAEDPYKKKHSRFKKPILFYESHVGISSEGKILYRISPW
AKYVYRENNUNVYDWIHMAPEDPYKKKHSRFKKPRSLRIYESHVGISSEGKILAYRISPW
AKYVYRENNUNVYDWIHMAPEDPYKKKHSRFKKPRSLRIYESHVGISSEGKILAYRISPW
HAYVYRSHONLOVINGYNCIOLMAIMEHAYYASFGYQITSFFAASSRYCTFEELKELVDTA
HSMGIVVLLDVVHSHASKNSEDGLNMFDGTDSCYFHSGPRGTHDLWDSRLFIYSSWEV
LRFLLSNIRWMLEEYCFDGFRFDGVTSMLYHHMGMGGFSGDYNLYFGLQVDEDALIY
LMLANHLAHTLYPDSITIAEDVSGMPALCSPTSQGGGGFDYRLAMAIPDKWIQLKEF
KOEDWINGGNIVTITNRYLEKCVAYAESHDQALVGOKTLAFWLMDAEMYTNNSVLAP
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FNLTDDDLLRYKFLNNFDRDMNRLEERCGWLSAPQAYVSEKHEANKTITFERAGLLFI
FNFHPSKSYTDYRVGTATPGKFKIVLDSDAAEYGGHQRLDHNTNYFAEAFEHNGRPYS
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                                    2133 atgcaagagtttgatcaagcaattcagcatcttgaagaagcctatggtttcatgacttct 2192
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Clemson University Genomics Institute
Clemson University
Clemson, SC 29634, US
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HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
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Unpublished (2000)
On Aug 21, 2000 this sequence version replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 864 656 7288 Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
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quality sequence stop: 679.
                                                Conservative
                                                                                                                                                              /Clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVDNA0009 (5 to 45 DAP)" /tissue_type="5-45 DAP Spike" /lab_host="SOLR" /lab_host="SOLR" /note="Vector: lambda2AP; Site_1: EcoR1; Site_2: Xho1" a 132 c 186 g 216 t 3 others
                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare"
/cultivar="Morex"
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
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On Jun 26, 2000 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0089P20f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
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76.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Matches 517;
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                                                                                                                                                                                                           15
  atttggacaccccgagtggattgattttccaagaggtgatctacatcttcccagtggtaa 2047
                                                                                                                          CATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCATAGCATTACATAAAAT 134
                                                                                                                                                catggctcttgacagaccatctactcctctcatagatcgtggagtagcattgcacaaaat 1927
                                                                                                                                                                                                         GATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTAATTTCATGGGAAATGA 194
                                                                 gatcaggcttattaccatgggattaggcggagaaggatatttgaattttatgggaaatga 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV_CEb0022L05f Hordeum vulgare seedling green leaf EST li
HVcDNA0005 (Erysiphe infected & control) Hordeum vulgare
HV_CEb0022L05f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 731.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for barley genomics 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF065047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                               Similarity
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="HV_CEb0022L05f"
/clone_lib="Hordeum vulgare seedling green leaf EST
/clone_Lib="Hordeum vulgare seedling green leaf EST
/library HVcDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: lambdaZAP; Site_1:
    167 c    212 g    226 t
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74.8%;
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Pred. No. 1.9e-104;
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green leaf EST library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAGGTGATCATCTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAA 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCAGATTTTCTTAGATATCGTGGTATGCAAGAGTTCGATCAGGCAATGCAGCATCTTGA
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                                                                                                          Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                            Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW596011 589 bp mRNA EST 18-JUL-2000 Si96903.yl Gm-c1032 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1032-269 5' similar to TR:Q41058 Q41058 STARCH BRANCHING ENZYME
                          High quality sequence stop: 407
                                                             info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1770 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycine max
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                                                                                                                                                                                                                                                                                                                         314 286 1800
314 286 1810
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                                                                                                                                                                                   atgggaaatgaatttggacaccccgagtggattgattttccaagaggtgatctacatctt
CCTAATGGCGTAGTAGTTCCAGGGAATAACAACAGTTTTGACAAGTGCAGGCGTAGATTT 370
                                                                                                                                             ATGGGGAATGAATTCGGCCATCCTGAGTGGATTGATTTCCCAAGGGGTGATCAACATCTT
                                                                                                                                                                                                                                                                                                                                        ttgcacaaaatgatcaggcttattaccatgggattaggcggagaaggatatttgaatttt 1976
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                                                                                                                                                                                                                                                                                          TTGCACAAAATGATTAGGCTTATTACCATGGGCCTTGGTGGAAGGGTATTTAAATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=28 and 8 respectively). This library was constructed by Dr. Pa Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in with cloned Pfu DNA, ligated to BCORI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNASe. NASE-Iree water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 500 bp cutoff, using GibcobRL Life Technologies' cDNA Size Fractionation column. The column eluent was then precipitated, redissolved, and ligated into Stratagene's CDNA str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 8-day-old 'Williams' seedlings which were propagated on paper towels with distilled water for 3 days (etiolated), then greenhouse grown for 5 days in potting soil. The cotyledons were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 100% of the white and 87.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' of the primer [GAGAGAGAGAGAGAGAGAGACTAGTCTGGAG(T)18V] anchor the primer at the 5' end of the poly(A) tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    After second strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
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/clone_lib="Gm-c1032"
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/db_xref="taxon:3847"
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Best Local
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ATAGAAGGTGGCTNGAGAAGTGTGTAACTTATGCAGAAAGTCATGATCAAGCACTAGTTG
                                                                                                                                                        486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Oglhara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSR7153 ITEC PSR Wheat Pericarp/Testa cDNA clone PSR7153, mRNA sequence.
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Norfolk, Norwich NR4 7UH UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Bailey P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: paul.bailey@bbsrc.ac.uk
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticeae;
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                        /Clone_lib="ITEC PSR Wheat Pericarp/Testa Library"
/tissue_type="pericarp/testa"
/tev_stage="3:1 mix 10:20 days post anthesis"
/dev_stage="1 mix 10:20 days post anthesis"
/note="vector: Lambda ZAP II (Stratagene)"
111 c 164 g 189 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Novosibirskaya
/db_xref="taxon:4565"
/clone="PSR7153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
/cultivar="Novosibirskaya 67"
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                                                                                                                                                                               Score 400.2; DB 16
Pred. No. 5.3e-101;
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                                                                                      /organism="Zea mays"
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CTTCGGAGCACCAATTCATATCACGAAA
                   cttctgagcaccaatacatatcacggaa 2215
                                                                          GCGGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGA
                                                                                              atggaatgcaagagtttgatcaagcaattcagcatcttgaagaagcctatggtttcatga 2187
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A samizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana:
of 12,028 non-redundant expressed sequence tags from nor
size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20363093
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1: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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six-week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="aboveground organs"
/dev_stage="two to six-week old"
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/clone="APZ36d06_r"
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tctggcaacaaagattctattcctgcttggatcaagttctcagttcaagcaccaggtgaa
                                                         GCAGATGGTACATCACCTATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATACTCCA
                                                                             gcagatggttcaccaccaattccccatggttctcgagtaaagatacgcatggatactcca 809
                                                                                                                                                          aatgcagatgtcatgactcagaatgagtgtggtgtctgggagatcttttttgccgaataat 749
                                                                                                                                                                                                              gagtgggcaccaggagctacgtgggctgcattgattggagatttcaataactggaatcct 689
                                                                                                                                   AATGCAGATCGTATGAGCAAAAATGAGTTTGGTGTTTGGGAAATTTTTCTGCCTAACAAT 184
                                                                                                                                                                                                                                                                                       TTCTCCCGTAGTTATGAGAAGTTTGGATTTAATCGCAGCGCGGAAGGTATCACATATCGA 64
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1 (bases 1 to 639)
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650 725 8221
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/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="B. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
/site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
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/db_xref="taxon:4577"
/cione_lib="687 - Early embryo from Delaware"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Appels R
Div. of Plant Industry,
Canberra ACT 2601 AUSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G. R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE402623 592 bp mRNA EST 21-JUL-2000 CSB009H05F990908 ITEC CSB Wheat Endosperm Library Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                  http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                       International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rudi@pi.csiro.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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61 62 465000
  D)
                                          /note="Vector: Lambda Zap/Bluescript; Site_1: XhoI;
Site_2: EcoRI; Plants grown in Phytotron with 18C/13C
(day/night) 16 hour light. MI3 Reverse sequencing primer
                                                                                                                      /tissue_type="endosperm"
/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
                                                                                                                                                                                                                               /db_xref="taxon:4565"
/clone="CSB009H05"
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                    /clone_lib="ITEC CSB Wheat Endosperm Library"
                                                                                                                                                                                                                                                                                 /cultivar="Wyuna"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tctacatcttcccagtggtaaatttgttcctgggaacaattacagttatgataaatgccg 2086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGCAATGCAGCATCTTGAGGAAAAATATGGGTTTATGACATCTGAGCACCAGTATGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCAACTTCCACTGGAGCAATAGCTTTTTTGACTACCGTGTTGGGTGTTCCAAGCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATGATGTCTACTTCACAACCGAACATCCGCATGACAATAGGCCACG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG551002 433 bp mRNA EST 09-APR-2001 sad31h09.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1074-1914 5' similar to TR:Q9XIS5 Q9XIS5 BRANCHING ENZYME 1
                                                                            Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                   Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                      BG551002.1
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Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1789 atgotgaaagtoatgaccaggocottgttggtgacaaaactattgcattttggctgatgg 1848
                                                                                                                                                                                                                                                                                                                                                 1909 gagtagcattgcacaaaatgatcaggcttattaccatgggattaggcggagaaggatatt 1968
                                                                                                                                                                                                                                                                                                    123 AAATGGGTGATATTGTCCACACATTAACAAACAGAAGGTGGCTGGAAAAATGTGTAGCTT
                                                                                                                                                                                          183 ATGCTGAAAGTCATGACCAGGCCTTGGTTGGTGACAAGACAATTGCATTTTGGTTGATGG
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                                                                                     ACAAGGATATGTATGACTTCATGGCTTTAGACAGACCATCCACACCTATTATAGATCGTG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             info@genomesystems.com web site: www.genomesystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the biunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DHIOB host cells. Plant care, incculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue with Pseudomonas syringae pv. glycinea carrying the avrB gene (Genetics 141:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mrNA pooled equally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR (hypersensitive response) by vacuum infiltrating plant
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/clone_lib="Gm-c1074"
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Pred. No. 3.1e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: oandersn@pw.usda.gov
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Contact: Olin Anderson
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The structure and function of the expressed portion of the wheat
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91 c 121 g 138 t
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/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
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/db_xref="taxon:4565"
/clone="WHE0803_A06_B11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 TCACCATGGGTTTAGGTGGCGAAGGCTATCTTAACTTCATGGGAAATGAGTTTGGGCATC 251
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                                                                                                                                                                                                                                                                                                        855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                Stanford University
                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
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                161
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                                                                                                                                                                                                                                                                     605011
                                                                                                                                                                                                                                                                                    walbot@stanford.edu
                D
                              /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
lab"
                                                                                     /tissue_type="nucellar, embryo, and endosperm"/dev_stage="10-14 days post-pollination"/lab_host="DH5(alpha)"
                                                                                                                                  /db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
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/cultivar="Ohio43"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2062 acaattacagttaatgataaaatgccggcgtaggtttgatctaggcaattcaaagcatctga 2121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2302 accqaqttqqctqcttaaaqccaqqaaaqtacaaqataqtcttqqattcaqatqatcctt 2361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGAAAAGGGAGATTTGGTATTTGTGTTCAACTTCCACTGCAACAACAGCTATTTTGACT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGATAATAGGCCATATTCGGTC 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKFZp43402123_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43402123 5', mRNA sequence.
                                                                            Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemann@kKrz heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 734)
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                                                                                                                                                                                                                                   EST (Blum, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                             Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                       Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                     Contact: Blum H
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
No s1 sequence available. This clone (DKFZP43402123) is available at the RZPD in Berlin
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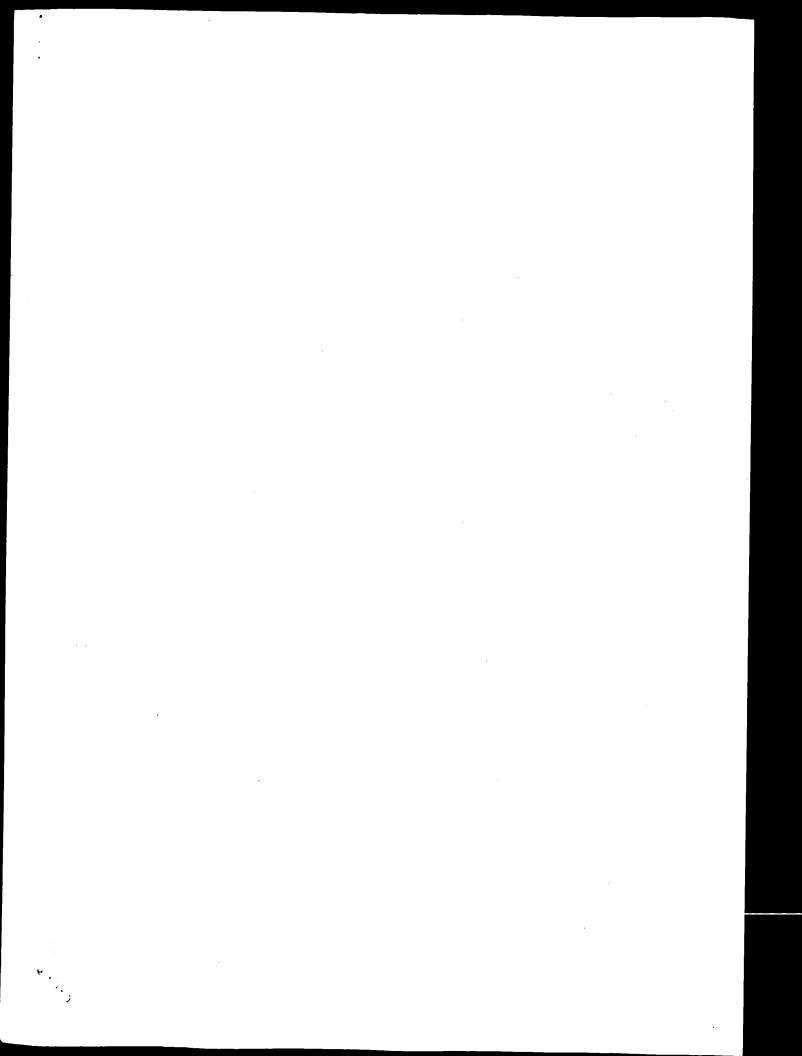
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FEATURES
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                                                                                                                              1765 ggtggttggaaaagtgtgtttcttatgctgaaagtcatgaccag 1808
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                                                                                                          AI993785 601 bp mRNA EST 08-SEP-1999
701514536 A. thaliana, Ohio State clone set Arabidopsis thaliana
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/tissue_type="testis"
/dev_stage="adult"
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AUTHORS
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KEYWORDS
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                    1995 caccccgagtggattgattttccaagaggtgatctacatcttcccagtggtaaa 2048
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428 CATCCAGAATGGCTTGATTTTCCCAGGACCCACGCAGGGCCTCTCAGCCGCACA 481
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4633 World Parkway Circle, St. Louis, MO 63134, USA
Fax: 314-427-3324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: service@genomesystems.com.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
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OM nucleic - nucleic search, using sw model
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AAT42632 AAT42637 AAC45939

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AAT42634

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I Jobling SA, Saliord K; X R WPI; 1998-286958/25. R P-PSDB; AAW62599.	(NATT) NAT STARCH & C	x 05-NOV-1996; 96GB-0023095.	Y 04-NOV-1997; 97WO-GB03032.	A 14-MAY-1998.	x W09820145-A2.	H Key Location/Qualitiers T CDS 21251 T /*tag= a /product= SBE II	Manihot esculenta.	Starch branching enzyme; SBE; cassava; ss.	Full length cassava tuber cDNA in pSJ107.	21-SEP-1998 (first entry)	AAV38719;	SULT 1 .V38719 AAV38719 standard; cDNA; 2913 BP.	ALIGNMENTS	8 18 AAT797	3 370.4 12.7 984 21 AAZ999	1 373.6 12.8 979 21 AAQ546 2 373.6 12.8 12151 15 AAQ546	0 376.2 12.9 1085 21 AAZ999	9 376.8 12.9 12151 15 AAQ621	7 384.8 13.2 8119 21 AA2333 8 376 8 12.9 977 21 AA2999	546.8 18.8 1865 18 AAT697	5 546.8 18.8 1809 18 AAT697	592.4 20.3 2713 19 AAV709	2 605.2 20.8 3128 16 AATOO7	0 625.2 21.5 2687 20 AAX346.	627 21.5 2733 15 AAQ621	633.4 21.7 2771 13 AAQ2429 633.4 21.7 2772 18 AAT697	633.4 21.7 2763 19 AAV297	633.4 21.7 2487 18	789.4 27.1 1452 21 AAC3695	1095.4 37.6 2165 18 AAT6973	1098.4 37.7 2087 18 AAT6973	1194.8 41.0 1919 19 AAV3872	1251.8 43.0 2665 to AA10972 1251.8 43.0 2725 19 AAV2975	1256.6 43.1 2640 19 AAV7096	1298 44.6 2919 15 AAV/3/3	1341.2 46.0 2975 17 AAT4263

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Best Local :
781 ctcgagtaaagatacgcatggatactccatctggcaacaaagattctattcctgcttgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2913 BP; 818 A; 549 C; 680 G; 866 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 4; 67pp; English.
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                                                                                     9f9fcf9g9agafctffffgccgaafaafgcagafg9ffcaccaccaaffccccafg9ff
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Pred. No. 0;
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potato

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Qy

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RESULT
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                     A cDNA clone (AAT69587) codes for potato starch branching enzyme II (BEII) (AAW19113). It was isolated from potato tuber cDNA by PCR amplification using primers (AAT69588-89) based on tryptic peptides of isolated BEII; the 5' and 3' ends of the sequence were detd. by RACE. A vector comprising the whole or a functional active part of the isolated sequence (sense or antisense), plus regulatory sequences active in potato, can be used to produce transgenic potatoes. The starch obtd. from such plants will show a changed pattern of amylopectin branching and an altered amylopectin/amylose
                                                                                                                    Isolated potato starch degree of amylopectin k potato starch
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(KHOS/)
(LARS/)
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29-NOV-1995;
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LARSSON H.
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Query Match

47.58;

Score 1384;

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                                ggtgtacacaccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaa 2506
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                                                                                                                                                                                           Best Local Similarity 77.3
Matches 1677; Conservative
                                                                                                                                                                                                                                                                             Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;
                                                                                                                                                                                                                                                                                                            Class A starch branching enzyme (SBB) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols.
                                                                                                                                                                                                                                                                                                                                                                              Claim 32; Page 55-56; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sidebottom CM, Westcott RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class A starch branching enzyme (psbe2con.seq - clone pSJ90).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amylose; viscosity; potato; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-506170/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1996;
467 agatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagtacaaaag 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW06400
                                                 410 tgataggatcagagagggggcatccctccacctggacttggtcagaagatttiitgaaat 469
                                                                       407 aattygatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 466
                                                                                                                      350 tggtaaactggaggagtctaaaacattaaatacttctgaagagacaattattgatgaatc 409
                                                                                                                                        347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
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95GB-0009229.
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                                                                                                                                                                                           47.4%; Score 1381.2; DB 17; Length 2578; 77.3%; Pred. No. 0; 43; Indels 0; 41.54
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols. This sequence was obtained by direct sequencing of PCR fragments amplified from first strand cDNA. Nucleotides which could not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 9; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
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05-MAY-1995;
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703 tcggaatgaatttggtgtctgggagatttttctgccaaataatgtggatggttctcctgc
               707 tcagaatgagtgtggtgtctgggagatctttttgccgaataatgcagatggttcaccacc
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95GB-0009229
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76.68;
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                          1787 ttatgotgaaagtoatgaccaggocottgttggtgacaaaactattgcattttcgctgat 1846
                                                                                                                                                                                                                                                                                                                     1603
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                                                                                                     gagagtgggtgatattgttcatacactgacaaatagaagatggtcggaaaagtctgtttc 1782
                                                                                                                                  gaaaatgggtgacattgtacatatgctgaccaacaggcggtggttggaaaagtctgtttc 1786
                                                                                                                                                                                                       gctgcatatggcaattgctgataaatggattgagttgctcaagaaacgggatgeggattg
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                                                                                                                                                     amylose;
                                                                                                                                                                 Starch branching enzyme; SBE; class
                                                                                                                                                                                           Class A starch branching enzyme (psbe2con.seq).
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                                                                                                                                                    viscosity; potato;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols.

The same sequence is given in Figure 8, however, nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New potato plant starch having high amylose content - also class starch branching enzyme and corresp. DNA to alter the viscosity starch; for use in food, biodegradable products, adhesives, etc.
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05-MAY-1995;
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                             atactatgatcctcccgaggaggaggaagtatgtgttcaaaaaatcctcagccaaagagacc
                                                                                                                                                                                                                                                         aattccccatggttctcgagtaaagatacgcatggatactccatctggcaacaaagattc
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atattatgatccacccgaagaggaggtatgtcttccaacacccacggccaaagaaacc
                                                                                                               cattcctgcttggatcaactactctttacagcttcctgatgaaattccatataatggaat
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76.18;
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Pred. No. 0;
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                                            2156 ggacaaggatatgtatgattttatggctttggatagaccgtcaacatcattaatagatcg 2215
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New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of
                                                               WPI; 1996-506170/50.
                                                                                             Sidebottom CM, Westcott RJ;
                                                                                                                                                                 (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                        10-APR-1996;
05-MAY-1995;
                                                                                                                                                                                                                                                                                                           07-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1997 (first entry)
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Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain is found, which is not found in class B mols.

Example 1; Page 49-51; 142pp; English

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                                                                                                         New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                            WPI; 1996-506170/50.
                                                                                                                                                                                                                              Sidebottom CM, Westcott RJ;
                                                                                                                                                                                                                                                                                        (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2511 ttggaacctgtcgccggttaagatatatcttaacaacaggttctgaagcaggaatgccat 2570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2413 tccgcggagtttttcacctctgatggaaggcacgataggccttgctccttmatggtg 2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2293 aacttccactggaccaacagttactctgactaccgtatcggttgctctgttcc::ggaaag 2352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2271 aattttcattggactagcagctattcggattaccgagttggctgcttaaagccaggaaag 2330
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05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9634968-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amylose; viscosity; potato; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class A starch branching enzyme (86con.seg) cloned in QE32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT42636 standard; DNA; 2576 BP
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                                                                                                                                                                                                                                                    Debet M,
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                                                                                                                                                                                                                                                    Gidley MJ, Jobling SA, Safford
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Sox

Sequence

2576

BP; 770

A; 462

C; 615

G; 729 T;

0 other;

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Best Local Similarity
Matches 1675; Conserv
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                                                                                                                                                                                                                                                                                                               aaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaa
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accacggggtcatcattggatgtgggactctcgccttttcaactatgggagctgggaggt 1366
                                                                                                                                                                                    cacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctacaatgc 1066
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                                        taatacgttggatgggctgaatatgtttgatggtacggatggtcactactttcactctgg
                                                                             taaagctcatgagctaggaattgttgttctcatggacattgttcacagccatgcatcaaa
                                                                                           taaagctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaac
                                                                                                                                    aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaaataga 1186
                                                                                                                                                                                                                                             ctcatacgtgaattttagagatgaagttcttcctcgcataaaaaagcttgggtacaatgc
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                          taatactttagatggactgaacatgtttgacggcaccgatagttgttactttcactctgg
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Pred. No. 0;
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2446	7 tcatgatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttcat	238	Qγ
w		w	Dβ
2386	7 aaagtacaagatagtettggatteagatgateetttgtttggaggetttggeagget	232	Qγ
2327	8 ctttaattttcactggacaaaaagctattcagactatcgcataggctgcctgaagcctgg	226	Дb
2326	7 attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccag	226	Qy
2266 2267	7 a 8 a	220	. Db
2207	gggctatgcagtatcttgaagataaatatgag1	214	Db
2206	.caagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaataca		Qγ
2147	graggrītgarcraggcaarīcaaagcarcrgagararca 	208	B 45
, 0	transarchicheogytylaasarcheythologyaaaccaathoaythatyakaastyca acaacacotototyatyactoaytaathoocyyaaaccaathoaythatyataaatyca acaacacotototyatyactoaytaathoocyyaaaccaathoaythatyataaatyca	202	D
0	8 cctaaatttcatgggaaatgaattcggccaccctgagtggattgatt	196	Db
2026	ttgaattttatgggaaatgaatttggacaccccgagtggattgatt	196	Qy
9	8 tgggatagcattgcacaagatgat		η 1
<u>ة</u> و	8 ggacaaggarargrargarrrrarggcrcrggaragaccgccaacarcarcaraaragac 7 tqqaqtaqcartqcacaaaatqatcaqqcttartaccatqqqartaqqcqqaqaaqaaqat	90	0 5
1906	ggacaaggatatgtatgacttcatggctcttgacag	84	VQ V
1846 1847	tattgcat tatagcat	7	Дb
1786 1787	ggt - gat	172 172	Ωу
1726 1727	ttgctgataaatgggttgagat ttgctgataaatggattgagtt	99	Db Qy
9 9	cagtttgcattcoggttgaagatggtggtgttggc 	160 160	Qy Db
1606 1607	it – ltg	54	Ф
1546 1547	aatactttggatatg aatactttggactcg	48 48	Ф
1486 1487	ttcaatgatgtacacccatcatggattgcaggtagat 	142 142	Фр
1426 1427	tctaaggtttcttctttcaaatgcaaggtggtggttggatgagtacaagtttgatg 	36	ФФ
1367	8 agctcgtggttatcattggatgtgggattcccgcctttttaactatggaaactgggaggt	130	Db

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872

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Matches 1685;
                                                                                                                                                                                                                                                                                                Class A starch branching enzyme (SBE) has been obtained potatoes. In class A SBE mols., a flexible N-terminal c
                                                                                                                                                                                                                                          Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;
                                                                                                                                                                                                                                                                     potatoes. In class A SBE MOIS, a LICALULE. is found, which is not found in class B mols.
                                                                                                                                                                                                                                                                                                                                                                 Claim 28-30; Page 42-46; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooke D, Debet M, Gidley MJ, Sidebottom CM, Westcott RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1996;
05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                      starch; for use in food, biodegradable products, adhesives, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-506170/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
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  407 aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 466
                                           573 tggtaaactggaggagtctaaaacattaaatacttctgaagagacaattattgatgaatc 632
                                                                                   347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
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Similarity 75.9%;
                                                                                                                                 Conservative
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95GB-0009229.
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145..288
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289..2
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                                                                                     1427 cagatttgatggggtgacttcaatgatgtacacccatcatggattgcaggtagattttac 1486
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New potato plant starch having high amylose content - also class starch branching enzyme and corresp. DNA to alter the viscosity starch; for use in food, biodegradable products, adhesives, etc.
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                                              ccagtcagctgccctcattggggatttcaacaattgggácgcaaatgctgactttatgac
                                                          tacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatgtcatgac
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                                                                                                                                  1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 40-41; 142pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class A starch branching enzyme (SBE) has been obtained potatoes. In class A SBE mols., a flexible N-terminal is found, which is not found in class B mols.
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The rice starch branching enzyme is encoded by the cDNA sequence AAQ73750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants.
                                                          Claim 1; Page 9-12; 13pp; Japanese.
                                                                                       New gene of branching enzyme of rice starch - useful for increasing starch yield of rice grains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                              92JP-0291719
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323..2606
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2603..2919
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Matches 1592;
                                                       1427 catcattggatgtgggattctcgccttttcaactatgggaattgggaagttctaagattt 1486
                                                                                1317 catcattggatgtgggactctcgccttttcaactatgggagctgggggggttctaaggttt 1376
                                                                                                                                                           1307 gagcttggtttagttgttgctcatggatgttgttcacagccatgcgtcaaataatacccta 1366
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1377 cttctttcaaatgcaaggtggttggttggatgagtacaagtttgatgggttcagatttgat 1436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 aaaccaaggtccattcctccacccggcagagggcaaagaatatatgacataga:ccaagc 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777 ggttctcgagtaaagatacgcatggatactccatctggcaacaaagattctaticctgct 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        827 tttggtgtttgggagatttttctgcctaacaatgctgatggctcatctcctati:ccacat 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 tgtggtgtctgggagatctttttgccgaataatgcagatggttcaccaccaccaat;ccccat 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              707
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                                                                                                                                                                                                                                                                                                                            gagttaggtcttcttgttctcatggatattgttcatagccatgcatcaactaa!acgttg 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaaccacntatgcc 1016
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1607

1497

1487

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aatgaatactttggatatgcaactgatgtagatgctgtgggtttatttgatgctgttgaat
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ccatgtagaacagcagtggtctatgctttagtggaggatgaa
                                              gagcacttcactgccgattgttcacatgacaacaggccctactcgttctcagtttattct
                                                                gtggtcttggactcagatgctggactctttggtggatttggcaggatccatcacactgca
                                                                                                                              atagtcttggattcagatgatcctttgtttggaggctttggcaggcttagtcatgatgca
                                                                                                                                                                    cattggagtaacagctattttgactaccgtgttggttgtttaaagccagggaaatataag
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                                                                                                                                                                                                                                                                                 Query Match 44.4%;
Best Local Similarity 76.3%;
Matches 1589; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch is improved by the use of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Pages 5-8; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            high quality starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice starch branching enzyme gene – synthesises amylopectin to yield
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(MITK ) MITSUI
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                                                                                                                                                                                                                                     416 taaaccaaggtccattcctccacccggcagagggcaaagaatatatgacatagatccaag 475
 656
                                                                                               692
                                                                                                                                                          632
                                752
                                                                                                                                                                                                                    572 taaaccacgagttatcccaccaccaggagatgggcagaagatataccaaattgacccaat 631
                                                                                                                                                          gctggaaggatttcggaaccatcttgactaccgatacagtgaatacaagagaatgcgtgc
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 tgcattgattggagatttcaataactggaatcctaatgcagatgtcatgactcagaatga
                               attcacccgcagcgctgaaggcattacctaccgagaatgggcacctggagcacagtctgc
                                               agaaattgacaagtatgaaggtagtctggatgcattttctcgtggctatgaaaagtttgg
                                                                                                                                                                           cttgacaggctttcgtcaacacctagattaccggtattcacagtacaaaaggactccgaga
                                                                                            agctattgaccaacatgaaggtggcttggatgcattttctcgtggttacgaaaagcttgg
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129..287
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288..2651
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129..2654
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                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                 Score 1292.6;
Pred. No. 0;
0; Mismatches
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23-AUG-1999 (first entry)
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03-APR-1998;
                                                                                                       Non-glycogen-like polysaccharide production; fermentation;
starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
non-starch branching gene; amylopectin; amylose; plant-lik: starch;
                        15-OCT-1998.
                                              W09844780-A1
                                                                       zea mays.
                                                                                             maize branching enzyme II; ss.
                                                                                                                                                           DNA encoding maize branching enzyme II.
98WO-US06660.
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04-APR-1997;

97US-0042939

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with
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Search completed: August 10, 2001, 12:53:48 Job time: 6670 sec

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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    DΒ
US-08-941-445A-14
US-09-087-277-3
US-08-941-445A-16
US-08-911-449-1
US-08-91-104-158-1
US-08-981-803-29
US-08-981-803-29
US-08-983-440-29
US-08-204-655B-1
US-08-204-655B-3
US-08-204-655B-7
US-08-470-702-2
US-08-470-702-2
US-08-467-831-2
US-08-467-831-2
US-08-467-831-3
US-08-276-652A-25
US-08-276-652A-25
US-08-276-452A-25
US-08-798-744-24
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Sequence 1, Appli sequence 3, Appli sequence 16, Appli sequence 1, Appli sequence 29, Appli sequence 3, Appli sequence 3, Appli sequence 14, Appli sequence 14, Appli sequence 17, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 2, Appli sequence 1, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 3, Appli sequence 2, Appli sequence 25, Appli sequence 25, Appli sequence 25, Appli sequence 26, Appli sequence 27, Appli sequence 27, Appli sequence 27, Appli sequence 28, Ap
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34	34	ω. ω.	34	34	34	34	34	34.6	34.6	34.6	34.6	34.6	35	35	35	ω 51	37
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Sequence 7,	Sequence 5,	Sequence 3,	Sequence 1,	Sequence 7,	Sequence 5,	Sequence 3,	Sequence 1,	Sequence 44	Sequence 54	Sequence 7,	Sequence 3,	Sequence 53	Sequence 9,	Sequence 9,	Sequence 2,	Sequence 1,	Sequence 1,
, Appl	Appl	Appl	Appl	, Appl	, Appl	, Appl	, Appl	1, App	1, App	, Appl	. Appl	3, App	, Appl	, Appl	. Appl	, Appl	, Appl

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/087.277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER: OF SEQ ID NOS: 4
COMMADER: DESCRIPTION NUMBER: SE 9601506-0
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SEQ ID NO 1
LENGTH: 3074
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APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: EK, BO
APPLICANT: KHOSNOODI, Jamshid
                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
          NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa =
OTHER INFORMATION: or Phe.
                                                                                                                                                NAME/KEY: misc_feature LOCATION: (92)..(2156) COLORITION: (92)..(2156) COTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are OTHER INFORMATION: n wherein n = A, C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Unknown Organism:bell gene OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide LOCATION: (189)..(332)
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (189)..(2825)
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; LOCATION: (2154)...(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro
US-09-087-277-1
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LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino
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OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
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OTHER INFORMATION: Amino acid 366 is Xaa wherein
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1067 tgttcagctcatggctattcaagagcattcatattatgctagtttttgggtatcacgtcac 1126
                                                                          1277 ctcatacgtgaattttagagatgaagttcttcctcgcataaaaaagcttgggtacaatgc 1336
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
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                                                                                                                                                                                       TELEFAX: (303) 499-808 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                         TOPOLOGIE TYPE: mx
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: BC
STATE: C
COUNTRY:
                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 30-SEP-1997
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   NAME/KEY:
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Best Local Similarity
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FEATURE:
NAME/KEY:
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                                                   TAGTTCTCATGGATGTGGTTCATAGTCATGCGTCAAGTAATACTCTGGATGGGTTGAATG
                                                                                                          GTTTTGGTACCCCAGAAGATTTGAAGTCTTTGATTGATAGAGCACATGAGCTTGGTTTGC
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1330 gggactotegoctttcaactatgggagctgggaggttctaaggtttcttcttctaaatg 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 1389 | 
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2345 CCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCACGCAGCCGAGCACTTCACCG 2404
                                                             2350 cagatgatcctttgtttggaggctttggcaggcttagtcatgatgcagagcacttcagct 2409
                                                                                                                                                                                                                                                                                                                                                   2290 gctattcggattaccgagttggctgcttaaagccaggaaagtacaagatagtcttggatt 2349
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                                                                                                                                                                                                                                                      2285 GCTATTTTGACTACCGTATTGGTTGTCGAAAGCCTGGGGTGTATAAGGTGGTCTTGGACT 2344
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                                                                                                                                                                                   Matches 1113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
UNMBER: OF SEQ ID NOS: 4
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APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature LOCATION: (424)..(1150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Unknown Organism:beII gene fragment OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum OTHER INFORMATION: (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (890)...(892)
OTHER INFORMATION: Amino a
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Nucleotide OTHER INFORMATION: C, G or T.
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                                                                                                                                                                                                                                                                                                                                                                 FEATURE: NAME/KEY: misc_feature LOCATION: (1148)..(115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (890)..(892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (422)..(424)
OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (422)..(424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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797 catggatactccatctggcaacaaagattctattcctgcttggatcaagttct:agttca 856
                                                                                                     737 tttgccgaataatgcagatggttcaccaccaattccccatggttctcgagtaangatacg 796
                                                                             1 tctgccaaataatgtggatggttctcctgcaattcctcatgggtccagagtgaigatacg 60
                                                                                                                                                                                                     Match 32.5%; Score 947.4; DB 4; Local Similarity 79.9%; Pred. No. 4.2e-281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotides 424, 891 and 1150 are n wherein n = A,
                                                                                                                                                                                      0; Mismatches 280; Indels
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ggatagaccntcaacatcattaatagatcgtgggatagcattgcacaagatgattaggct
                     tgacagaccatctactcctctcatagatcgtggagtagcattgcacaaaatgatcaggct 1936
                                                                                                              tgagattattcagaagagatgaagattggaaaattgggtgacattgtacatatgctgac 1756
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                                                                                                                                                                                                                                                                                                           TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Keeling, Peter
APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                              FEATURE:
                                                                                             LOCATION: FEATURE:
                                                                                                                                             FEATURE:
                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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1208 TTGGATGAATTCATGTTTGATGGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1267
                                   1401 ttggatgagtacaagtttgatgggttcagatttgatggggtgacttcaatgatgtacacc 1460
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; Sequence 1, Application US/08716449
; Patent No. 6103893
; GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation

US-08-716-449-1

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2135 CTGGTCTTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCA 2183
                                         2358 cctttgtttggaggctttggcaggcttagtcatgatgcagagcacttca 2406
                                                                                                2075 GGCTACAAAGTGGGATGGGATTTGCCTGGGGAAATACAGAGTAGCCCTGGACTC%GATGCT 2134
                                                                                                                                            2298 gattaccgagttggctgcttaaagccaggaaagtacaagatagtcttggattcugatgat 2357
                                                                                                                                                                                                 2015 GTCTTTGAACGTGGAGATTTAGTTTTTGTTTTCAATTTCCATCCCAAGAAAACCTACGAG 2074
                                                                                                                                                                                                                              2238 gtcttcgagaggggaaacctcgtttttgtattcaattttcattggactagcagctattcg 2297
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                                                                                                                         IDENTIFICATION METHOD: lone ORF with homoly indentification METHOD: branching enzymes OTHER INFORMATION: complements KVB32 E. CO. OTHER INFORMATION: branching enzyme mutant US-08-716-449-1
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                                                        Matches 1138;
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/GE
FILING DATE: 22.03.95
ATTORNEY/AGENT INFORMATION:
NAME: Anita E.Nador
REGISTRATION NUMBER: 1
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: IMB 1.44 MB High Density Diskette
COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible
COMPUTER: WINDOWS 95
COMPRATING SYSTEM: WINDOWS
     419
            540 attgacaagtatgaaggtagtctggatgcattttctcgtggctatgaaaagtttggtttc 599
                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                          POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: | ANTI-SENSE: NO
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TELEPHONE: (416) 368-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                               MMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                           SATURE: open reading frame NAME/KEY: starch branching enzyme LOCATION: 44-2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 CLONE: 1.2.1 and E2
                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
                                                                     Local Similarity
                                                                                                                                                                                                                                    UNITS:
                                                                                                                                                                                                                                                            CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                               ORGANELLE
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DEVELOPMENTAL STAGE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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ATTGAAAAATATGAGGGACCCCTTGAGGAATTTGCTCAAGGTTATTTAAAATTTGGATTC 478
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Box 194, 24th Floor, Toronto-Dominion Bank Tower
                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding starch branching enzyme
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                                                                    20.8%;
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                                                                                                                                               DD: branching enzymes complements KV832 E. coli glycogen
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                                                                                                                                                                                                                                                                                                                                                                                                mature tuber
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                                                Score 605.2; DB 3,
Pred. No. 1e-175;
""smatches 693;
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1602 gatgitagiggaatgccaacagittgcattccggitgaagatggtggtgttggctitgat 1661
1376 TITACAGGAAACTATAATGAGTATTTCAGCGAGGCTACAGATGTTGATGCTGTGGTCTAT 1435
                                                                                                                                                                                                                                                                                                                   1482 tttaccggcaactacaatgaatactttggatatgcaactgatgtagatgctgtgggtttat 1541
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                                                                                                                                  TTAATGTTGGCCAATAATCTGATTCACAAGATTTTCCCAGACGCAACTGTTATTGCCGAA 1495
                                                                                                                                                                         ttgatgctgttgaatgatatgattcatggtctcttcccagaggctgtcaccattggtgaa 160:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCGTGAGTTTGCAGATGATGTTTTACCTCGGATTAAGGCAAATAACTATAATACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaacaca 1010
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                                                                                                     APPLICANT: KOSSMANN, Jens
APPLICANT: Mueller-Roeber, Bernd
APPLICANT: Visser, Richard Gerardus Francisus
APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: CANSHIDS CONTAINING DNA-SEQUENCES THAT
TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1943 AAATGTAGACGCCAGTGGAACCTCGCAGATAGCGAACACTTGAGATACAAGTTTATGAAT 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2183 TTGCCAGGGAAGTACAGAGTTGCACTGGGCAGTGATGCTTGGGAATTTGGTGGCCATGGA 2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2063 CAGATAGTAAGCAGCATGGATGATGATAATAAGGTTGTTGTGTTTGAACGTGGTGACCTG 2122
                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                     NUMBER OF SEQUENCES:
                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caatacatatcacggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctc 2258
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                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                     Sonnewald,
                                                                                                                                                                                                                                                                                                                        Willmitzer, Lothar
                                   Ostrolenk, Faber, Gerb & Soffen
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US-08-104-158-1
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TELEX: 236925
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP P FILING DATE: 11-FEB-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ker
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELLING CO... 800
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
EP_CT/EP92/00302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULL | NO HYPOTHETICAL: NO
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COUNTRY:
ZIP: 10
                                                                                                                                                                                                                                                                                                                                                                  540 attgacaagtatgaaggtagtctggatgcattttctcgtggctatgaaaagttt:ggtttc 599
                                                                                                                                                                                     660 ttgattggagatttcaataactggaatcctaatgcagatgtcatgactcagaa~gagtgt 719
                                                                                                                                                                                                                                                                                  600 tcacgcagtgaaacaggaataacttatagagagtgggcaccaggagctacgtgggctgca 659
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE - Defection
780 tctcgagtaaagatacg---catggatactccatctggcaacaaagattctattcctgct 836
                                                                                       720 ggtgtctgggagatcttttgccgaataatgcagatggttcaccaactaccaattccccatggt 779
                                                                                                                                                                                                                                         299 AACAGGGAAGATGGTTGCATAGTCTATCGTGAATGGGCTCCTGCTGCTCAGGAAGCAGAA 358
                                                                                                                                                                                                                                                                                                                                      239 ATTGAAAAATATGAGGGACCCCTTGAGGAATTTGCTCAAGGTTATTTAAAAATT::GGATTC 298
                                                 419 GGTGTTTGGAGTATTAGAATTCC---TGATGTTGACAGTAAGCCAGTCATTCCACACAAC 475
                                                                                                                                           FILING DATE:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOCITIES TYPE: TULL TUBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: growing tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: New York TRY: U.S.A. 10036-8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H: 2909 base pairs
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(partial) truncated protein; 97,11 % identity to
active potato branching enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 587.8; DB 4; Length 2909; Pred. No. 2.1e-170;
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                                                                                          TGTATAGCATATGCGGAGAGCCATGATCAGTCTATTGTCGGTGACAAGACCATTGCATTT
                                                                                                                            tgtgtttcttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattt 1838
                                                                                                                                                                                                             GAAGATTGGTCCATGAAGGAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGAAG
                                                                                                                                                                                                                                                                                                                                 TACCGCCTGGCAATGGCAATCCCCAGATAAGTGGATAGATTATTTAAAGAATAAGAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATTTCGATTTGATGGAATAACTTCTATGCTGTATGTTCATCATGGAATCAATATGGGA 1195
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TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 67459-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-14
EARLIER FILING DATE: 1995-07-14
NUMBER: 0F SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Solanum tuberosum US-08-981-803-29
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                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 29
LENGTH: 11478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/08981803 Patent No. 6147279 GENERAL INFORMATION:
                                                                                                                                                                                           Matches 590;
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
                                                                                   5242 acaggtaccacttcaaataccctcgccctcccaaaccccgagccccacgaatctatgaag 5301
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                   970 cgcacgttggaatgagtagtacggagccagtaattaacacatatgccaactttagagatg 1029
                                                                                                                910 agaagtatgtgttcaaaaatcctcagccaaagagaccaaaatcacttcggatttatgagt 969
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                         Score 369; DB 3;
Pred. No. 8.5e-103;
                                                                                                                                                                                   Mismatches 315;
                                                                                                                                                                                                                            Length 11478;
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Sequence 29, Application US/08983440
Patent No. 6232122
GENERAL INFORMATION:
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              APPLICANT: POULSEN, Peter
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674599-2003
CURRENT ELIZATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER APPLICATION NUMBER: POT-14
EARLIER FILING DATE: 1995-07-14
EARLIER FILING DATE: 1996-07-12
EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(11478)
OTHER INFORMATION: K stands for G or T/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(11478)
OTHER INFORMATION: R stands for G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: W stands for A or T/U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: M stands for A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: variation LOCATION: (1)..(114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5242 acaggtaccacttcaaataccctcgccctcccaaaccccgagccccacgaatctatgaag 5301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1150 gatttggaactcctgatgatttaaagtctctaatagataaagctcacgagttaggtcttc 1209
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1501 aatactttggatatgcaactgatgtagatgctgtggtttatttgatgctgttgaatgata 1560
                                                   5782 taacttctatgctgtatgttcatcatggaatcaatatgggatttacaggaaaccataatg 5841
                                                                                 1441 tgacttcaatgatgtacacccatcatggattgcaggtagattttaccggcaaccacaatg 1500
                                                                                                                                                       5722 tttccaacttgaggtggtggctagaagagtataactttgacggatttcgatttgatggaa 5781
                                                                                                                                                                                        1381 tttcaaatgcaaggtggttggttggattgagtacaagtttgattgggtttgatgggt 1440
                                                                                                                                                                                                                                                           5662 ataagttgtgggatagcaggctgttcaactatgccaattgggaggttcttcgtttccttc 5721
                                                                                                                                                                                                                                                                                            1321 attggatgtgggactctcgccttttcaactatgggagctgggaggttctaaggfttcttc 1380
                                                                                                                                                                                                                                                                                                                                                               5602 gctttgatattggccaaggttctcaagaatcctactttcatgctggagagcgauggtacc 5661
                                                                                                                                                                                                                                                                                                                                                                                                   1270 tgtttgat------ggtacggatggtcactactttcactctggaccacggggtcatc 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5482 gatatggaaacccggaggacctaaagtatctgatagataaagcacatagcttg;gtttac 5541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 369; DB 4; Length 11478;
64.3%; Pred. No. 8.5e-103; Indels 12; Gaps
tive 0; Mismatches 315; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08528026C Patent No. 6248566
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
LENGTH: 2426
TYPE: DNA
ORGANISM: Bacillus stearothermophilus (Strain TRBE14)
                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 9900-0002.20

CURRENT APPLICATION NUMBER: US/08/528,026C

CURRENT FILING DATE: 1995-09-13

PRIOR APPLICATION NUMBER: US 08/415,152

PRIOR FILING DATE: 1995-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (385)..(392)
OTHER INFORMATION: S SD sequence
NAME/KEY: misc_feature
LOCATION: (402)..(2357)
OTHER INFORMATION: P CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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1123 tcacaaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaa 1182
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                                             cgcacattgagttgcttcctctcgtcgagcatccgctcgaccgctcgtggggctatcaag 1014
                                                                              atgctgttcagctcatggctattcaagagcattcatattatgctagttttgggtatcacg 1122
                                                                                                            tttatacgtaccgtgagatggccgatgaactgatctcgtatgtgctcgatcatgggttta 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn version 3.0
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TAKATA, Hiroki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAKAHA, Takeshi
YANASE, Michiyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMANAKA, Tadayuki
TERADA, Yoshinobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUJII, Kazutoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKAMURA, Hiroyasu
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE SAM
                                                                                                                                                                                           2.3%;
                                                                                                                                                                              0;
                                                                                                                                                                                           Score 68.4; DB 4; Pred. No. 8.3e-11;
                                                                                                                                                                              Mismatches 231;
                                                                                                                                                                                                          Length 2426;
                                                                                                                                                                              Indels
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                                 US-08-232-463-14
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                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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COMPUTER: IF
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                                                  CLONE:
                                                                                   TOPOLOGY:
                                                                                                 STRANDEDNESS:
                                                                                                                 TYPE:
                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313-0299
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GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                               TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                           TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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1800 Diagonal Road,
                                                                                                                                                      (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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single
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US-08-204-656B-1
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                              TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                            REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Metho
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Falls Church
STATE: Virginia
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                                                                                                                                                                                             Weiner, Marc S.
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1404 base pairs
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                                                                                                                                                                                                                                      02-MAR-1994
N: 435
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US-08-204-656B-3
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TELEFAN. (703) 205-80
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/204,656B FILING DATE: 02-MAR-1994 CLASSIFICATION: 435
                                                                          REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
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ANTI-SENSE: NO
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LOCATION: 1.1404
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                               NAME: Weiner, Marc
REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nuclei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Birch, Stewart, Kolasch & Birch, LLP 8110 Gatehouse Road, Suite 500 East
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                                                                                                                                                                  Marc S.
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                                                                                                                                            32,181
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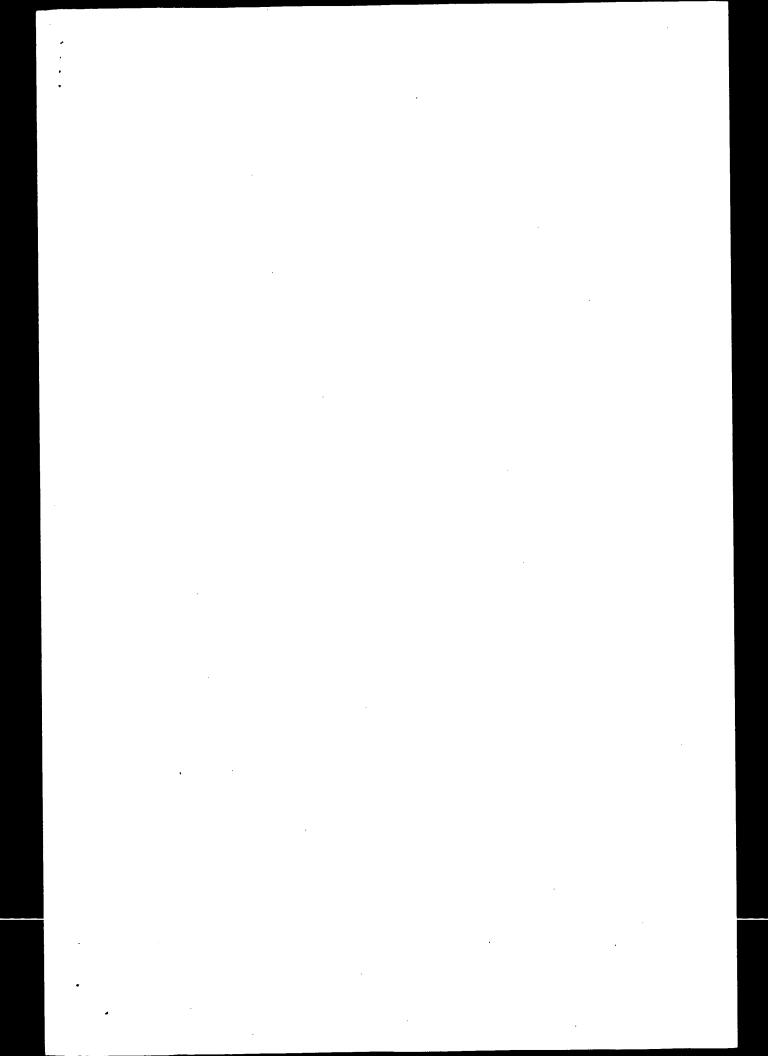
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic nucleic acid"
                REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
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                                                                          ATTORNEY/AGENT INFORMATION: NAME: Weiner, Marc S.
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church
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Local Similarity 56.1%;
mes 78; Conservation
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OTHER INFORMATION:
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LOCATION: 1..1404
                                                                                                                                   APPLICATION NUMBER: US/08/204,656B FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE:
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                                                        REGISTRATION NUMBER:
                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TELEPHONE:
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correspond to nucleotides 79-1482 in
fibuligera `-amylase structural gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08470702 Patent No. 5631149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.4%;
Best Local Similarity 56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                  FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1160 tcctgatgatttaaagtctctaatagataaagctcacgagttaaggtcttcttgttctcat 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1220 ggatattgttcatagccat 1238
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ANTI-SENSE: NO
                FILING DATE: 02-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1..1404
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 GGATATCGTTACCAACCAT 369
                                                                                                                                                                                                                                                                                                                            STREET: 8110 Gateho CITY: Falls Church
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STRANDEDNESS:
                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                 APPLICATION NUMBER: US/08/470,702
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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WEINER, MARC S.
                                                                                                                                                                                                                                                                                     Virginia
Y: U.S.A.
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8110 Gatehouse Road,
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MIYAIRI, SACHIO
HONDA, KOICHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        correspond to nucleotides 79-1482 of the Saccharomycopsis fibuligera `amylase structural gene"
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                                                                                                                                                                          Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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; MOLECULE TYPE:
; HYPOTHETICAL: I
; ANTI-SENSE: NO
US-08-470-702-1
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US-08-470-702-2
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                   APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC: S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
                                                                                                                                                                                                                                         ZIP: 22042
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/470,702
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REFERENCE/DOCKET NUMBER: 237
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1220 ggatattgttcatagccat 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 TGCTGATGATTTGAAGTCTTTGGCACAAGAATTGCACGATCGTGATATGTTGTTAATGGT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match 1.4%; Score 41.4; DB 1; Length 1404; Local Similarity 56.1%; Pred. No. 0.012; nes 78; Conservative 0; Mismatches 61; Indels 0;
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(703) 205-8000
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TELEX: 248345
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                             Ouery Match 1.4%; Score 41.4; DB 1; Length 1434; Best Local Similarity 56.1%; Pred. No. 0.012; Matches 78; Conservative 0; Mismatches 61; Indels 0;
                                                                            | 1100 ttatgctagttttgggtatcacgtcacaaacttttatgcagctagcagccgatttggaac 1159
                       1220 ggatattgttcatagccat 1238
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                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
351 GGATATCGTTACCAACCAT 369
                                                                                                                                                              231 TTATGCTTATCATGGTTGGTGGATGAAGAACATATACAAAATTAATGAAAACTTTGGTAC 290
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Search completed: August 10, 2001, 12:49:44 Job time: $6506\ sec$



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Database :
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.Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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  1344157 seqs, 7733874588 residues
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2913
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90 : : : 921 : : : 944 : : : 955 : : : 957 : : : 987 : : : 987 : : : 987 : : : 987 : : : 987 : : : : 987 : : : : 987 : : : : : : 987 : : : : : : 987 : : : : : : 987 : : : : : : 987 : : : : : : 987 : : : : : : 987 : : : : : : 987 : : : : : : : 987 : : : : : : : 987 : : : : : : : 987 : : : : : : : : 987 : : : : : : : : : : : : : : : : : : :	72: 73: 74: 75: 76: 76: 77: 78: 78: 78: 77: 78: 77: 78: 78: 78	58: 60: 62: 63: 64: 65: 65: 67: 69:	444444000000000000000000000000000000000
gb_pr4:* gb_pr5:* gb_pr6:* gb_pr7:* gb_pr7:* gb_pr8:* gb_pr9:* gb_r01:* gb_in4:* gb_pr10:* gb_pr10:* gb_pr10:*		vil viz viz htg htg htg htg htg	em_ov:* em_pat:* em_pat:* em_pl:* em_pl:* em_sts:* em_sy:* em_sy:* em_vi:* em_vi:* gb_sts::* gb_sts::* gb_sts::* gb_sts::* gb_sts::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 2913 2028 1475.2 1467.4 1396.4	Query Query Match Length DB 100.0 2913 9 50.6 3549 14 50.4 3360 12 47.9 2517 12	Length: 2913 3090 3549 3360 2517	DB 9 9 9 14 12 12 12 12	ID A92162 A92164 PSSBEIGEN AB029548 AB029548	Description A92162 Sequence 28 A92164 Sequence 30 X80009 P.sativum m AB029548 Phaseolus AB042937 Ipomoea b
o 20 ↦	2913 2028	100.0	2913 3090	99	92162 92164	A92162 Sequence A92164 Sequence
٠ ،	14/5.2	50.6	3549	14	PSSBEIGEN	X80009 P.sativum
n #	1307.4	50.4	3360	12	AB029548	AB029548 Phaseol
חנ	1300.4	4.	7757	7	AB042937	AB042937 Ipomoea
1 C	1392.4	1 0	2542	14	ATU22428	U22428 Arabidop
	1364.8	4/.5	2493	15	STSBEII	AJ000004 Solanii
a	1382.8	41.5	2523	15	STU011889	AJ011889 Solanu

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                    source
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1251.8
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Sequence 28 from Patent
A92162
                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 2913)
Safford, R. and Jobling, S.A.
IMPROVEMENTS IN OR RELATING TO STARCH CONTENT OF PLANTS
Patent: WO 9820145-A 28 14-MAY-1998;
SAFFORD RICHARD (GB); JOBLING STEPHEN ALAN (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
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A58167 Sequence 18
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SOURCE

TITLE

VERSION

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Sequence 30 from Patent W09820145. A92164 A92164.1 GI:6740960

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58	attgatctt	caggaatg	caggttctgaa	gatatatettaaca	cgccggtta	2521	Qy	
52	TTGGAACCTG	TITITITITI		AGTGGTCTATGCTTT	GTAGAACAGCA	2461	Db	
52	ttggaacctg	gtggagaatgaa	gtggaggatgaa	tggtctatgcttt	tagaacago	2461	Qy	
6 6	TACACACCAT		TAACCGGCCTCGA		ACTTCAGCTTT	2401	Db	
6	tacacaccat	tccttcatggi	taaccggcctcga	gaagggtggtacga	cttcac	2401	Qy	
40	ATGATGCAGAGC	CAGGCTTAGTCAT		AGATGATCCTTTGTTT	TCTTGGATTCA	2341	Db	
4	qatqcaqaqc	aggcttagtcat	ggaggctttgg	gatgatcctttc	cttggatt	2341	Ωу	
2340	TACAAGATAG		AGTTGGCTGCTT		GGACTAGCAG		Db	
	+	a a contra a	agttggctgc+;	attoggattaco	gactagcac	2281	VΩ	
20 1	AATTTTCATT	GETTTTGTATTC			AAAGGGATCG	.2221	DЬ	
သ ၂	aattttcat	qttttqtattc	aggggaaacc	cattgtcttcc	gggatcg	2221	Qy	
22	CGGAAGGATG		GACTTCTGAGO	AGCCTATGGTTTCAT	ATCTTGAAGAA	2161	DЬ	
22	cggaaggat	aatacatatca	gacttctgago	gcctatggtttca	tcttgaag	2161	Qy	
16			TCATGGAATGC	AAAGCATCTGAGATA	TAGGCAATTC	2101	Db	
16	gcaattcag	agagtttgatca	tcatggaatgo	aagcatctgac	aggcaatto	2101	Qy	
10	TAGGTTTGATC			TGTTCCTGGGAACAA	GTGGTAAATTT	2041	Db	
10	aggtttgat	taaatgccggcg	ttacagttatga	gttcctgggaa	gtggtaaa	2041	Qy	
04	ACATCTTCCCA	CAAGAGGTGATCTA		TGGACACCCCGAGTG	GAAATGAATT	1981	DЬ	
04	catcttccc	aagaggtgatc	gattgattttco	ggacaccccgag	gaaatgaatt	1981	Qy	
1980	GAATTTTATGG	AGAAGGATATTT	:ATGGGATTAGGCGG	AGGCTTATTACC	ACAAAATGATC	1921	Db	

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REFERENCE
AUTHORS
TITLE
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531 AAAGTGAATCTAAACCAAGGTCCATTCCTCCACCTGGCAGTGGGCAGAATATATGACA 590
                                            406 aaattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgaca 465
                                                                                                                                         471 TTGAGGAGGATGAAGTAAAAAAGAGTCGGTTCCATTGCATGAGACAATTAGCATTGGAA 530
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Safford,R. and Jobling,S.A.
SMETONIEMENTS IN OR RELATING TO STARCH CONTENT OF PLANTS
PATENT: WO 9820145-A 30 14-WAY-1998;
SAFFORD RICHARD (GB); JOBLING STEPHEN ALAN (GB)
LOCATION/Qualifiers
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                          1486 ccggcaactacaatgaatactttggatatgcaactgatgtagatgctgtggtttatttga 1545
                                                                            1551 TTAGATTTGATGGGGTGACTTCCATGATGTACACTCCCCATGGGTTGCAGGTAGCTTTTA 1610
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                                                  ATATGAGATTGATCCACTTTTGCAAGCTCACCGTCAGCATCTTGATTTCCGTTATGGACA 782
                                                                                                atatgacatagatccaagcttgacaggctttcgtcaacacctagattaccggtattcaca 517
                                                                                                                                                              CAAGAAAGTAAAAGTAGATAAACCTAAGATCATTCCTCCACCCGGTACTGGGCAGAAAAT 722
gtacaaaagactccgagaagaaattgacaagtatgaaggtagtctggatgcattttctcg 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JUL-1994) R.A. Lane, Norwich NR4 7UH, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burton, R.A.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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argityremapgaksallygdrnwhaddyntkdafgweifelpnnadgsppiphg
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riyeshapgaksallygdrnwhaddyntkdafgweifelpnnadgsppiphg
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ffapsspfglafduelyvymklyndlithglfpraysigedysmynthglqd
gsrgyhmmdsrlfnygdwelylkyllfglfpraysigedysmynthglgdy
sftgnyssyfglatduelyvymklyndlithglfpraysigedysmynghpfclpy
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/protein_id="CAA56319.1"
/db_xref="GI:1345570"
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/clone_lib="cDNA_LAMBDA_gt11"
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ggctt 	8 tgaagatgttagtggaatgccaacagtttgcattccggttgaagatggtggtgtt	y 159	γo
attg ATTG	8 ttatttgatgctgttgaatgatatgattcatggtctcttcccagaggctgtcacc 	y 153 o 180	pb Qy
	8 agattttaccggcaactacaatgaatactttggatatgcaactgatgtagatgct 		ОР
caggt CAGGT	8 tgatggttcagatttgatggggtgacttcaatgatgtacacccatcatggattg 	y 141 o 168	p
aagtt AAGTT	8 ctgggaggttctaaggtttcttctttcaaaatgcaaggtggtggttggatgagtac 	y 135 o 162	Db Qy
gggag GGAAG	8 tcactctggaccacggggtcatcattggatgtgggactctcgccttttcaactat.	y 129 o 156	40 40
ACTT	8 tgcatcaactaatacgttggatggctgaatatgtttgatggtacggatggtcact 	7 123 5 150	DP 60
lgcca - - GCCA	8 totaatagataaagotoacgagttaggtottottgttotcatggatattgttcata 	7 117 5 144	d d
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IGGTA	8 ctacaatgctgttcagctcatggctattcaagagcattcatattatgctagttttg 	, 105 5 132	B 8
ttgg	8 agtaattaacacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagc 	, 99) 126	ρ γ
agcc AGCC	8 aaagagaccaaaatcacttcggatttatgagtcgcacgttggaatgagtagtacgg 	, 93) 120	dd Ao
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cata CATA	8 caaagattctattcctgcttggatcaagttctcagttcaagcaccaggtgaactcc 	10	Ωy
gcaa GGAT	8 ttcaccaccaattccccatggttctcgagtaaagatacgcatggatactccatctg 	102	Qу
atgg ATGG	8 tgtcatgactcagaatgagtgtggtgtctgggagatctttttgccgaataatgcag 	96	ОУ
caga CAGA	8 accaggagctacgtgggctgcattgattggagatttcaataactggaatcctaatg 	63 90	ОУ
999c	8 tggctatgaaaagtttggtttctcacgcagtgaaacaggaataacttatagagagt 	57 84	оу Об
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2763 TGAATCAGAGCCAATTGAACTGTCAGATGGAGTAGA 2798
                               2498 agtggagaatgaattggaacctgtcgccggttaaga 2533
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                                                                                                                                             2643 TAGGCTCAATCATACTGCTGAGTACTTCACCTCTGAAGGGTGGTATGATGACCGGCCTCG
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                                                                                                                                                                                                                                   2523 GGTCTTTGTCTTCAATTTTCACTGGACCAACAGTTATTCAGATTACAAGGTTG(CTGTTT 2582
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                                                                   ATCTTTCCTCGTTTATGCACCTTCTAGAACAGCAGTGGTGTATGCCCTTGCGG/ATGGAGT 2762
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RESULT AB029548 LOCUS DEFINITION ACCESSION KEYWORDS VERSION ORGANISM AB029548.1 GI:5441245

AB029548 3360 bp mRNA pLN 10-JUL-1999 Phaseolus vulgaris kbel mRNA for branching enzyme 1 complete cds. branching enzyme 1.
Phaseolus vulgaris cDNA to mRNA.
Phaseolus vulgaris
Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;

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AUTHORS
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 ACAATTTGGCTTCCTACGCAGTGCTACAGGCATTACTTATAGAGAGTGGGCACCTGGAGC
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Fax:81-11-706-3635)
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GFMTTEHQYISRKNEGDKVIIFERGNLVFVFNFHWNNSYSDYRVGCATPGKYKIVLDS
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                                                       tagtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttgattatcg
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                     Starch-branching enzyme cDNA from sweet potato (Ipomoea batatas) published Only in DataBase (2001) In press 2 (bases 1 to 2517) Abe, J. and Oricht, T. Direct Submission
Submitted (18-MAY-2000) Jun-ichi Abe, Kagoshima University, Faculty
                                                                                                                                                                                                                                                                                                                                              Ipomoea batatas IBE mRNA for starch branching enzyme, partial cds. aB042937
                                                                                                                                                                               Magnoliophyta; eudicotyledons; core en I; Solanales; Convolvulaceae; Ipomoea
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Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GGGTGGCTTGGAAGTATTCTCTCGTGGCTATGAGAAATTAGGTTTCACTCGGA;TGCTAC
          481 GTACAAATTTCAACATCCACGGCCAAAAAGACCAAAGTCACTGAGAATATATGAATGTCA 540
                                  914 gtatgtgttcaaaaatcctcagccaaagagaccaaaaatcacttcggatttatgagtcgca 973
                                                                                                  421 ACAAGCTCCTGGTGCAATTCCTTATGATGGAATATACTATGATCCTCCAGAAG%GGAGAG 480
                                                                                                                                          854 tcaagcaccaggtgaactcccatataatggcatatactatgatcctcccgaggaggagaa 913
                                                                                                                                                                                         361
                                                                                                                                                                                                                    794 acgcatggatactccatctggcaacaaagattctattcctgcttggatcaagtictcagt 853
                                                                                                                                                                                                                                                                                                                                                                            674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 aggtagtotggatgcattttctcgtggctatgaaaagttttggttttctcacgcagtgaaac 613
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                                                                                                                                                                                                                                                                                                              CTCTTTGCCAAACAATGCAGATGGCTCACCTGCAATTCCACATGGCTCTAGAGTGAAGAT 360
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434 tccacccggcagaggcaaagaatatatgacatagatccaagcttgacaggctitcgtca 493
1 TCCACCTGGACTTGGTCAGAGGATCTATGAGATAGACCCTCTCTTGAAAAATTTTCGTGA 60
                                                                                                                                                              Match 47.9%;
Local Similarity 79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Agriculture; Korimoto 1-21-24, Kagoshima, Kagoshima 890-0065, Japan (E-mail:j_abe@chem.agri.kagoshima-u.ac.jp, Tel:81-99-285-8642)
                                                                                                                                   Conservative
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VESRGYEKLGFTRSATGITYREWAPGATWATILIGDENNWNPADDWTRNEFGWEISL
PNADGSBA IPHGSRYKIRMOTPSGIKDSIPAMINESYGAPGAIPYDGIYXIDPPEERI
YKFOHPRPKRPKSLRIYECHIGMSSEPPKINTYAERADDVLPHKKLGYNALQIMAIQ
YKFOHPRPKRPKSLRIYECHIGMSSEPPKINTYAERADDVLPHKKLGYNALQIMAIQ
LINEDGTJDSCYFHGGTRGAYHWMDSFRLENYGNREVLRYLLSAR-RWMLDETKFDGFRED
GYTSMMTTHHGLSVGFTGNYSEXFGYATDVDAVVLMLVNDLIHGFPEAITIGEDVG
VTSMMTTHHGLSVGFTGNYSEXFGYATDVDAVVLMLVNDLIHGFPEAITIGEDVG
SYAERGIEVNGGVFEDYRLHMAIDFXWIEILKRRDEBWOMGFITHTLINTRRHLEKVC
SYAESHDQALVGDKTIAFWLMDKDMYDDMALDRPATFVIDRGIAHKMIRLITMGLGG
EGYLNFMGNEFGHPEWIDFPRGEGREDGNESVLEGNNESVBKCIFRFDLGDADYLRYR
MGCLKFORAKWALDSDSPLFGGFGRVQPDAEFFTFEGYHDDRIRSFMYSTSDY
VGCLKFOKAKVALDSDSPLFGGFGRVQPDAEFFTFEGYHDDRIRSFMYDAPSRTAVVY
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1 487 c 59
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/cultivar="Joy White"
/db_xref="taxon:4120"
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/protein_id="BAB40334.1"
/db_xref="GI:13516907"
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TCACCCAGAGTGGATTGATTTCCCTAGAGGTGAACAACGCCTTCCTGATGGTTCAGTTCT
                                                                                                              gcttattaccatgggattaggcggagaaggatatttgaattttatgggaaatgaatttgg 1993
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                                                                                    ACTTATAACTATGGGATTAGGAGGAGAAGGATATCTAAATTTCATGGGGAACGAATTTGG
                                                                                                                                                                           TCTGGATAGACCAGCAACGCCAGTAATAGACCGTGGAATAGCATTGCATAAAATGATCAG
                                                                                                                                                                                                  tettgacagaccatetacteeteteatagategtggagtageattgcacaaaatgateag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcatctgagatatcatggaatgcaagagtttgatcaagcaattcagcatcttgaagaagc 2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGGATTACCGTGTAGGCTGCTTAAAGCCGGGAAAATATAAGGTAGCCCTGGACTCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thale cress.

Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2542)

1 (bases 1 to 2542)

1 (bases 1 to 2542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guilti
Two closely related cDNAs encoding starch branching
Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                               Submitted (09-MAR-1995) Dane K. Fisher, Horticulture, Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                   Fisher,D.K., Gao,M., Kim,K.-N., Boyer,C.D. and Guiltinan,M.J. Direct Submission
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U22428.1 GI:726489
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 2542)
                                                                                                                                                                                                                                                                                                                                                  University, 103
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6-alpha-d-(1,4-alpha-d-glucano)-transferase"
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                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                         .2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                starch
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BASE COUNT

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Best Local Similarity 79.0
Matches 1657; Conservative
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Best Local
                                                                                                                                        1060 acaatgctgttcagctcatggctattcaagagcattcatattatgctagttttgggtatc 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 ATGAGATAGACCCCATGTTACGAACTTACAACATCATCTTGATTACCGTTATGGACAGT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 TCAAGGAGAGAGGGTGAAACCAAGAATAGTTCCCCCCACCGGGTGATGGCAAGAAATTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   640 caggagctacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatg 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 gctatgaaaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcac 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 ATAAAAGATTGCGTGAAGAAATAGACAAGTATGAGGGTGGTCTTGAGGCATTCTCTCGTG 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 atgacatagatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagt 519
962 ATAATGCTGTTCAAATTATGGCCATACAAGAACATTCATATTATGCCAGCTTTGGGTACC 1021
                                                                                                                                                                                                                                                                                                  842 AGAGACCTAAGTCGCTAAGGATTTATGAAGCACATGTTGGCATGAGTAGCACGGAACCAA 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 662 CGCCTGCAATTCCTCATGGCTCACGTGTAAAGATTCGTATGGATACTCCATCTGGCATTA 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760 caccaccaattccccatggttctcgagtaaagatacgcatggatactccatctggcaaca 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 TCATGACTCGGAATGAATTTGGTGTTTTGGGAGATCTTTTTGCCCCAACACACTGATGGTT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 CTGGAGCTAAGGCTGCATCACTTATCGGAGATTTCAACAACTGGAATTCTAATGCAGATA 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   agagaccaaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccag 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atggcatatactatgatcctcccgaggaggaggagtatgtgttcaaaaatcctcagccaa 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGACTCAATTCCTGCTTGGATCAAGTTCTCGGTGCAAGCTCCAGGTGAAATCCCATTCA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagattotattootgottggatcaagttotoagttoaagcaccaggtgaactoccatata 879
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GYEKLGESRESDAGITYERBAPGAKAASLIGDENNWISSNADIWEN REGUEAFER
GYEKLGESRESDAGITYERBAPGAKAASLIGDENNWISSNADIWEN REGUEAFER
GYEKLGESRESDAGITYERBAPGAKAASLIGDENNWISSNADIWEN REGUEAFER
GSPALIPHGSRVKIRMDTPSGIKOSITAMIKESVOAPGEIPPNGIYYDPEBEKYVEK
DGSPALIPHGSRVKIRMDTPSGIKOSITAMIKESVOAPGEIPPNGIYYDPEBEKYVEK
HPOPPREKYLEY IYEHAVGESTEPMVNIYANFEDDVLPRIKKLGYNAVOLMAIGHEYY
YASIGCYHYMBYD FADSSCCOTPEBLKSLIDRAHELGIVVLMDIVHSHASKNITLDGLNNE
YASIGCYHWMWDSLELENYGSBUVLKYLLSVARWMLEXYKEDGFREDGVIS
MMYTHHGLSVGFTONYTEYFGLETDVDAVNYLMLVNOMIHGLYPEALTIVGEDVSGNFT
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FCIPVOBGCWGFDYRLHMAIAKWITELLIKKRDEDWNGDIYTTLTNRRWSEKCISYEE
SHDQALVGBGYGFTORLHMAIAKWITELLIKKNITELITNGLGGEGYL
NFMGNUEGHPEWID PRGECRLSDGSVIFGNUT VERGEDLYEVFNFHMTSSYFDYRIGGS
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KPGKYKIVLDSDDPLFGGENRLDRKAEYFTYDGLYDERPCSFNVYAPCRTAVVYALAN
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1120 acgtcacaaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctc 1179

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1502 AAGATGTTAGTGGTATGCCAACATTCTGTATTCCTGTCCAAGATGGTGGCGTTGGATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1600 aagatgttagtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttg 1659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1480 attttaccggcaactacaatgaatactttggatatgcaactgatgtagatgctg::ggttt 1539
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                                                                                                                                                                                                                                                                                                                1900 tagatcgtggagtagcattgcacaaaatgatcaggcttattaccatgggattacggcggag 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1840
2200 aatacatatcacggaaggatgaaagggatcggatcattgtcttcgagaggggganacctcg 2259
                                                       2042 AATTTGATCAGGCAATGCAACATCTTGAAGAGAATTACGGTTTTATGACTTCG(AGCACC 2101
                                                                                                                                                                                                             1922 GAGGCGAGCAGCGTCTTTCTGATGGTAGCGTGATTCCTGGCAACAATTTCAGTTATGACA 1981
                                                                                                                                                                                                                                              2020 gaggtgatctacatcttcccagtggtaaatttgttcctgggaacaattacagttatgata 2079
                                                                                                                                                                                                                                                                                        1802 TCGATAGAGGAATAGCTTTGCACAAAATGATTAGGCTTATAACTATGGGATTACGCGGTG 1861
                                                                                          2140 agtttgatcaagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcacc 2199
                                                                                                                                    1982 AATGCCGCCGCAGATTTGATCTTGGGGATGCAGATTATCTCAGATACCGCGGACTACAAG 2041
                                                                                                                                                                 2080 aatgccggcgtaggtttgatctaggcaattcaaagcatctgaggtatcatggaaitgcaag 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctgatggacaaggatatgtatgacttcatggctcttgacagaccatctactcctctca 1899
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Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum.
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Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H.
Molecular cloning and characterization of starch-branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell
Research, Genetic Center, Swedish University of Agricultura
Sciences, Box 7055, S-750 07 Uppsala, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSBEII 2493 bp
Solanum tuberosum mRNA
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Larsson, C.T.A.
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                                                    /db_xref="Sptremel:049953"
/translation="EKSSYNSESPSTVAASGKVLVPCTQSDSSSSSTDQFEFTETSP
/translation="EKSSYNSESPSTVAASGKVLVPCTQSDSSSSSTDQFEFTETSP
ENSPASTDVDSSTMEHASQIKTENDDVEPSSDLTGSVEELDFASSLQLQEGGKLEESK
TLNTSEETIIDESDRIEERGIPPGLGQKIYEIDPLLTNYRQHLDYRYGYKKLERAI
DKYEGGLEAFSRGYEKMGFTRSATGITYREWAPGAQSAALIGDFNNWDANADIMTRNE
FGVWELFILNNVDGSFAIPHGSRVKIRWDTPSGVKDSIPAWINYSLQLPDEIPYNGIY
                 YDPPEEERY IFQHPRPKKPKSLRIYESHIGMSSPEPKINSYVNFRDEVLPRIKKLGYN
AVQIMAIQEHSYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSH
{	t ASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEF}
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/protein_id="CAA03846.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /plasmid="pALSBE-II (#123)"
/cultivar="Amanda"
                                                                                                                                                                                        /db_xref="GI:2764396"
                                                                                                                                                                                                                                                                   function="branches 1,4-alpha glucans"
                                                                                                                                                                                                                                                                                                /EC_number="2.4.1.18"
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                                                                                                                                                                                                                                                                                                                                                           /gene="Sbe-II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4113"
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RRWSEKCVSYAESHDQALVGDKTIAFH
LVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDGSVIFGNQFSYDKGTRREDLGD
AEYLRYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHW
TKSYSDYRIGCLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYA
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                                                                                                                                                                                                                                       2085 CCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCAT
                                                                                                                                                                                                                                                                                                                                                                  2025 ACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGA
                                                                                                                                                      atcacggaaggatgaaagggatcggatcattgtcttcgagagggggaaacctcgtttttgt 2266
                                                                                                                                                                                                                                                                                                                                                                                                  TGGGAACTACAAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGAT 1484
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                                                                                                                       tcaagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaatacat 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAACACCTCTCTGATGGCTCAGTAATTCCCCGGAAACCAATTCAGTTATGATAAATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                totacatottoccagtggtaaatttgttoctgggaacaattacagttatgataaatgccg 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggagtagcattgcacaaaatgatcaggcttattaccatgggattaggcggagaaggata 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCATCAACATCATTAATAGATCG 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggacaaggatatgtatgacttcatggctcttgacagaccatctactcctctcatagatcg 1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTC 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaaaatgggtgacattgtacatatgctgaccaacaggcggtggttggaaaagtgtgtttc 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgaattggaacctgtcgccggttaagatatatcttaacaacagg 2550
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Jobling, S. A., Schwall, G.P., Westcott, R.J., Sidebottcm, C.M., Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum tuberosum I.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SFE II Unpublished
2 (bases 1 to 2523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jobling, S.A., Jobling, S.A., Plant Submitted (07-0CT-1998) Jobling S.A., Plant Submitted (07-07-000) John Market Submitted (07-07-000) Jobling S.A., Plant Submitted (07-07-000) Jobling Submitted (07-
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/Codon_start=1
//Codon_start=1
//protedi_id="starch branching enzyme II"
//protedi_id="starch branching enzyme II"
//protedi_id="CAB40747.1"
//brotedi_id="GI:4584511"
//db_xref="GI:4584511"
//db_xref="GI:4584511"
//translation="ILAEKSSYNSEFRESTVAASGKVLVPGT(;SDSSSSSTNOFEFTE
TSPENSPASTDYNSSTWEHASQIKTENDDVEPSSDLTGSVEEI.DFXSVQYKKLR
ESKTLWTSEGTIDESSRIRERGIPPGCLGVKYTEIDPLLTN:RGHLDYRYSQYKKLR
EAIDKYEGGLEAFSRGYEKMGETRSATGITYREWAPGAOSAAI.IGDFNNWDANDIMT
RNEFGYWEIFLENNVDGSPAIPHGSRVKIRMDTPSGVKDSIP;WINYSLQLPDEIPYN
GIYYDPPEERKYIFQHERPKKEKSLRIYESHIGMSSPEERIN;YVNFEDEVLPRIKL
GYNALOIMAIDEHSYYASFGYHYTNFFARAPSSRFGTPDDLKSL;DSAHELGIVYLMDIV
HSHASNNTLDGLNMFDGTDSCYFHSGARGYHWMMDSRLFNYGHWEVLRVILSNARWML
DEFKFDGFFFDGVTSMMYTHHGLSVGFFGNYEFFFGLATDVDÄVVYLMLVWDLIHGLF
PDAITIGEDVSGMFTGIPVODGGVGFDYRLHMAIADKWIELLKKRDEMWRVGDIVHT
LTNRRWSEKCVSYAESHDOALVGDKTIAFWLMDKDMYDEMALDRESTSLLDRGIALHK
MIRLYTMGLGGEGYLNFMGNEFGHPEWIDFPRAEOHLSDDSV::PGNQFSYDKCRRRFD
LGDAEYLRYGGGCGFGRAENDALDSDDPLFGGFGRIDHNAE::FTFEGWYDDRPRSIM
FHWTKSYSDYRIGCLKFGKYKVALDSDDPLFGGFGRIDHNAE::FTFEGWYDDRPRSIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="sequence SBE A-5" <2. .10
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/cultivar="Desiree"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SBE II"
<2. .2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name="1,4-alpha-Glucan branching enzyme"
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SBE II"
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taaagctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaac 1246
                                               tgttcagctcatggctattcaagagcattcatattatgctagtttttgggtatcacgtcac 1126
                                                                aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga
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CTTTAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGG
                                                                                 atcacggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctcgtttttgt 2266
                                                              ATCACGAAAGGATGAAGGAGATAGGATGATTGTATTTGAAAAAAGGAAACCTAGTTTTTGT
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707 tcagaatgagtgtggtgtctggggagatcttttttgccgaataatgcagatggttcaccacc
                                                     650 CCAGTCAGCTGCCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGAC 709
                                                                        647 tacgtgggctgcattgattggagatttcaataactggaatccttaatgcagatgtcatgac 706
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Cooke, D., Debet, M., Gidley, M.J., Jobling, S.A., Safford, F. Sidebottom, Christopher, M. and Westcott, R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION Patent: WO 9634968-A 19 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A.,
Sidebottom, Christopher,M. and Westcott,R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COM
Patent: WO 9634968-A 17 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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2383 TCATAATGCCGAATATTTCACCTCTGAAGGATCGTATGATGATCGTCCTCGTTCAATTAT 2442
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1136 CATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAAT 1195
                                                                                      1076 AATTCCTCATGGGTCCAGAGTGAAGATACGCATGGACACTTCATCAGGTGTTAAGGATTC 1135
                                                                                                                                                                          1016 TCGGAATGAATTTGGTGTCTGGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCCTGC 1075
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                      827 tattcctgcttggatcaagttctcagttcaagcaccaggtgaactcccatataatggcat 886
                                                                                                             767 aatteeeeatggttetegagtaaagataegeatggataeteeatetggeaacaaagatte 826
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COOKE, D., Debet, M., Gidley, M.J., Jobling, S.A., Safford, R., Sidebottom, Christopher, M. and Westcott, R.J.
IMPROVEMENTS IN OR RELATING TO PLANT: STARCH COMPOSITION Patent: WO 9634968 A 18 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
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COOKe.D., Debet,M., Gidley,M.J., Jobling,S.A.,
Sidebottom, Christopher,M. and Westcott,R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COM
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NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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Best Local Similarity Matches 1677; Conserv

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Score 1370.4; Pred.

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94	atactatgatcctcccqaggaggagaagtatgtgttcaaaaatcctcagccaaagagacc	887 888
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76 76	tcagaatgagtgtggtgtctgggagatctttttgccgaataatgcagatggttcaccacc	707 710
70	tacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatgtcatgac 	647 650
64	aaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcaccaggagc	587 590
5 5	actccgagaagaattgacaagtatgaaggtagtctggatgcattttctcgtggctatga 	527 530
5 5	agatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagtacaaaag	467 470
4 4	aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat	407 410
40	tyttgaagatgaagtaaataaagaatctyttccaatgcgggagacagttagcatcagaaa 	347 350

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tgaattggaa 2516	ggtgtacacaccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaa 2506	AATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTAT 244	atgatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttc	aaagtacaagatagtcttggattcagatgatcctttgtttg	TAATTTTCACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCC	tcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccag	ATCACGAAAGGATGAAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGT 2267	tcacggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctcgtttttg	CGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCAT 220	Colonia i Concentratori de la concentratori del concentratori del concentratori de la concentratori de la concentratori de la concentratori de la concentratori del concentratori del concentratori del concentratori del concentratori de la concentratori del conc	gcgtaggtttgatctaggcaattcaaagcatctgagatatcatggaaatgcaagagtttga 2146 	AACACCTCTCTGATGACTCAGTAATTCCCGGAAACCAATTCAGTTATGATAAATGCAG 208	cagtggtaaatttgttcctgggaacaatt	AAATTTCATGGGAAATGAATTCGGCCACCC	attttatgggaaatgaatttggacaccccgagtggattgatt	TAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGG	ggagtagcattgcacaaaatgatcaggcttattaccatgggattaggcggagaaggat		gacaaggatatgtatgacttcatggctcttgacagaccatctactcctcatagatc	ATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGAT 1847	atgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattttggctga	GAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAAGT3TGTTTC 1787	aaaatgggtgacattgtacatatgctgaccaacaggcggtggttggaaaagtgtgttt	THE THE TRANSPORT OF TH	ctccacatggctgttgctgataaatgggttgagattattcagaagagagatgaagatt	TAGCGGAATGCCGACATTTTGTATTCCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCG 1667	agtggaatgccaacagtttgcattccggttgaagatggtggtgttggctttgattatc		ctgttgaatgatatgattcatggtctcttcccagaggctgtcaccattggtgaagatg	TGGGAACTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGAT 1547	gcaactacaatgaatactttggatatgcaactgatgtagatgctgtggtttstttga	TGATGGTGACATCAATGATGTATACTCACCACGATTATCGGTGG 3ATTCA	gatttgatggggtgacttcaatgatgtacacccatcatggattgcaggtagatttt jj

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jobling, S.A.
Direct Submission
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Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure
cloning and characterisation of multiple forms of SBE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids; Solanales; Solanaceae; Solanum.
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Solanum tuberosum
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NVDGSFAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIYYDPPEERYI
PQHPREKKPKSVRIYESHIGMSSPEPKINSYVWFIEDEVLPRIKKLGYNAVQIMAIQEH
SYYASFGYHVTINFFAPSSRFGTPDDLKSLIDKAHELDEVLMDIYHSHASNNTLDGLN
MFDGTDSCYFHSGARGYHWMWDFRLENYGNWFVLRYLLSNARWHLDEFKFDGFRFDGV
TSMMCTHHGLSVGFTGNYEEYFGLATDVDAVVYLMLVNDLIHGLFPDAITIGEDVSGM
PTFCVPVQDGGVGFDYRLHMAIADKWIELLKKRDEDWRVGDIVHTLTNRRWSEKCVSY
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140 .2
                                                                                                                  /product="starch branching enzyme II" 529 c 703 g 862 t
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284. .2773
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VDKEEEEEEEEVAVVEEEVVVEEE"
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YLNEMGNEFGHPEWIDFPRAEQHLSDGSVIPRNQFSYDKCRRREDLGDAEYLRYRGLQ
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/EC_number="2.4.1.18"
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/protein_id="CAB40746.1"
/db_xref="GI:4584509"
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140. .2776
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/cultivar="Desiree"
/db_xref="taxon:4113"
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  47.08;
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ACTTAGGTATCTTCTCTCAAATGCGAGATGGTGGGTTGGATGAGTTCAAATTTGATGGATT 1647
                                                                                                     accaoggggtcatcattggatgtgggactctcgccttttcaactatgggaggttggggaggt 1366
                                                                                                                                                                                                                                        TAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGACATTGTTCACAGCCATGCATCAAA 1467
                                                                                                                                                                                                                                                                                                                      aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga 1186
                                                                           AGCTCGTGGTTATCATTGGATGTGGGATTTCCGCCTCTTTAACTATGGAAACTGGGAGGT 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcagaatgagtgtggtgtctgggagatctttttgccgaataatgcagatggttcaccacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAGCTTTTTCTCGTGGTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcatcagaaa 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1787 ttatgctgaaagtcatgaccaggcccttgttggtgacaaaactattgcatttttggctgat 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1888 GCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTG 1947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1828 TAGCGGAATGCCGACATTTTGTGTTCCCGTTCAAGATGGGGGTGTTGGCCTTTGACTATCG 1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1948 GAGAGTGGGTGATATTGTTCATACACTGACAAATAGAAGATGGTCGGAAAAGTGTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2147 tcaagcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaatacat 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2087 gcgtaggtttgatctaggcaattcaaagcatctgagatatcatggaatgcaagagtttga 2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2128 TGGGATAGCATTACACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAAGGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2068 GGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2008 ATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGAT 2067
   2668
                                                         2447
                                                                                                                  2608 TCATAATGCCGAATATTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTAT 2667
                                                                                                                                                   2387 tcatgatgcagagcacttcagctttgaagggtggtacgataaccggcctcgatccttcat 2446
                                                                                                                                                                                                                                                                  2327 aaagtacaagatagtcttggattcagatgatcctttgttttggaggctttggcaggcttag 2386
                                                                                                                                                                                                                                                                                                                                                                                           2267 attcaattttcattggactagcagctattcggattaccgagttggctgcttaaagccagg 2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2207 atcacggaaggatgaaagggatcggatcattgtctttggagaggggaaaccttgtttttgt 2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2368 CCGGGCTATGCAGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTCAT 2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2308 ACGGAGATTTGACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGA 2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2248 ACAACACCTCTCTGATGGCTCAGTAATTCCCCAGAAACCAATTCAGTTATGATAAATGCAG 2307
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                                                                                                                                                                                                                                 2548 AAAATACAAGGTTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAATTGA 2607
                                                                                                                                                                                                                                                                                                                                               2488 CTTTAATTTTCACTGGACAAAAGGCTATTCAGACTATCGCATAGGCTGCCTGAAGCCTGG 2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    totocacatggotgttgotgataaatgggttgagattattcagaagagagatgaagattg 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tggagtagcattgcacaaaatgatcaggcttattaccatgggattaggcggagaaggata 1966
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                              ggtgtacacaccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaa 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCACGAAAGGATGAAGGATAGGATGGATTGTATTTGAAAAAGGAAACCTAGTTTTTGT 2487
   GGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGTAGACAAAGAAGAAGAAGAAGA 2727
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Matches 1825;

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    Query Match
Best Local :
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-DEC-1994) Dane K. Fisher, Department of Horticulture, The Pennsylvania State University, Biotechnology Institute, 103 Tyson Building, University Park, PA 16802, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guiltinan,M.J.
Two closely related cDNAs encoding starch branching enzyme from
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core &udicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U18817.1 GI:619938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 30 (1), 97-108 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thale cress.
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(Strain="Columbia"
/db.xxef="taxon:3702"
/clone="Lambda IV-2-1; p421df"
/tissue_type="seedling hypocotyls"
/dev_stage="3 day-old seedling"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="sbe2-1"
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                              DDSAEFFTSDGRHDDRPCSFMVYAPCRTAVVYAAVDDDDDDERSSLVPIGLLPEDV"
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    Score 1366.6; DB 14; Length 2668; Pred. No. 0;
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	1191 gctcacgagttaggt	1131 ttttatgcagctagc 1141 TTTTTCGCACCTAGC	1071 cagctcatggctatt 1081 CAGATAATGGCCATT	.011 tatgccaactttaga	951 tcacttcggatttat 961 TCGCTGCGTATATAT	891 tatgatcctcccgag 901 TATGACCCTCCTGAG	831 cctgcttggatcaag 	771 ccccatggttctcga 781 CCCCATGGCTCCCGT	711 aatgagtgtggtgtc 721 AACGACTTTGGTGTG	651 tgggctgcattgatt 661 GCAGCATCACTGATC	591 tttggtttctcacgca 601 TTTGGCTTCACTCGAA	531 cgagaagaaattgac 541 CGTGAAGAAATTGAC	471 ccaagcttgacaggc	1 ggatctaaaccaagg 	80 aatgcgggaga 61 ACATCTGGAAG	324 agtctcattatggatg 301 GTTCAGAAAACTGAAG	264 gatcaattggaagccc 241 GATCAAGTACAATCTC	204 gtcactgcttctaaa 184 ACCACTGCATCTGAG	110000000000000000000000000000000000000
and which we have the contraction of the property of the contraction o	ttcttgttctcatggatattgttcatagccatgcatcaacta	gccgatttggaactcctgatgatttaaagtctctaatagata 	aagagcattcatattatgctagttttgggtatcacgtcac 	atgatgtgcttcctcgcatcaaaaagcttggctacaatgctg 	agtogcacgttggaatgagtagtacggagccagtaattaaca 	gaggagaagtatgtgttcaaaaatcctcagccaaagagaccaa 	totoagttoaagcacoaggtgaactoocatataatggcatat 	taaagatacgcatggatactccatctggcaacaaagattcta 	.gggagatctttttgccgaataatgcagatggttcaccaccaa 	gagatttcaataactggaatcctaatgcagatgtcatgactc 	gtgaaacaggaataacttatagagagttgggcaccaggagct 	agtatgaaggtagtctggatgcattttctcgtggctatç 	ttogtcaacacctagattaccggtattcacagtacaaaagac 	attcetccacccggcagagggcaaagaatatatgacatag 	tcagaaaaatt 	ataagattgttgaagatgaagtaaataaagaatctgtt 	ctggcacagtttcagaagaatcccaggtgcttactgatgttg 	tccttcctgatggtcggattgaatgctattcttcttcaa 	

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2330	aattttcattggactagcagctattcggattaccgagttggctgcttaaagccaggaaag 	2271	Qy
2270 2280	cggaaggatgaaagggatcggatcattgtcttcgagaggggaaacctcgtttttgtattc	2211 2221	рь
2210	gcaattcagcatcttgaagaagcctatggtttcatgacttctgagcaccaatacatatca	2151	Qy
2220		2161	Db
2150	aggtttgatctaggcaattcaaagcatctgagatatcatggaatgcaagagtttgatcaa	2091	ОУ
2160		2101	
2090 2100	catcttcccagtggtaaatttgttcctgggaacaattacagttatgataaatgccggcgt	2031 2041	ДУ
2030	aattttatgggaaatgaatttggacaccccgagtggattgatt	1971	Qy
2040		1981	Db
1970 1980	gtagcattgcacaaaatgatcaggcttattaccatggattaggcggagaaggatatttg	1911 1921	Qу
1910	aaggatatgtatgacttcatggctcttgacagaccatctactcctctcatagatcgtgga	1851	Дb
1920		1861	
1850 1860	gctgaaagtcatgaccaggcccttgttggtgacaaaactattgcattttggctgatgac	1791 1801	ДУ
1790 1800	atgggtgacattgtacatatgctgaccaacaggcggtggttggaaaagtgtgtttcttat	1731 1741	Qу
1730	cacatggctgttgctgataaatgggttgagattattcagaagagagatgaagattggaaa	1671	Db Qy
1740		1681	
1670 1680	ggaatgccaacagtttgcattcoggttgaagatggtggtgttggctttgattatcgtctc	1611 1621	Фр
1610 1620	ttgaatgatatgattcatggtctcttcccagaggctgtcaccattggtgaagatgttagt	1551 1561	ДУ
1550	aactacaatgaatactttggatatgcaactgatgtagatgctgtggtttatttgatgctg	1491	Qy
1560		1501	Db
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1500		1441	Db
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1440		1381	Db
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1380		1321	
1310	acgttggatgggctgaatatgtttgatggtacggatggtcactactttcactctggacca	1251	Qy
1320		1261	Db
1260		1201	DЬ

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FEATURES
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2341 TACAAAATCGTTTTGGACTCTGATAACTCTTTATTTGGAGGCTTCAACCGGCTAGATGAC 2400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCGCGGAGTTTTTCACCTCTGATGGAAGGCACGACGATAGGCCTTGCTCCTTCATGGTG 2460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacaagatagtcttggattcagatgatcctttgtttggaggctttggcaggcttagtcat 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacacaccatgtagaacagcagtggtctatgctttagtggaggatgaagtggagaatgaa 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jobling,S.A., Schwail,G.P., Westcott,R.J., Sidebottom,C.M., Bebet,M., Gidley,M.J., Jeffcoat,R. and Safford,R. A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure cloning and characterisation of multiple forms of SBE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-CCT-1998) Jobling S.A., Plant Science Unit, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                potato.
Solanum tuberosum
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SBEII gene; starch bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STU011890 2992 bp mRNA for starch branching enzyme II, sequence SBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jobling, S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="sequence SBE A-6" 140. .283
DESDRIRERGIPPPGLGQKIYEIDPLLTNYRQHLDYRYSQYKKLREAIDKYEGGLEAF
SRGYEKMGFTRSATGITYREWALGAQSAALIGDENWODANDLWIRNEEGVWEIFLPN
NVDGSPAIPHGSRVKIRMDTPSGVKDSIPAWINYSLQLPDEIPYNGIHYDPPEEERYI
FQHPRPKKPKSLRIVESHIGWSSPEPKINSYVNFRDEVLPRIKKLGYNALQIMAIQIM
SYYASFGYHVTNFFAPSSRFGTPDDLKSLIDKAHELGIVVLMDIVHSHASNNTLDGLN
                                                                                                                                            /translation="MYYTLSGYREPTYPSYYKSNGFSSNGDRNANVSYELKKHSLSR
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SSTMEHASQIKTENDDVEPSSDLTGSVEELDFASSLQLQEGGKLEESKTLNTSEETII
                                                                                                                                                                                                                                    /evidence=experimental
/product="starch branching enzyme II"
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/db_xref="GI:4584513"
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/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/cultivar="Desiree"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POCAL
                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SBE II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SBE II"
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BASE COUNT
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1067 tgttcagctcattggctattcaagagcattcatattatgctagtttttgggtatcacgtcac 1126
                                                                                                                1228 CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC
                                                                                                                                                                                                                                                                1168 AAAGTCGCTGAGAATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAAATTAA 1227
                                                                                                                                                                                                                                                                                                                                                                                                                   1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1048 CATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCCATATAATGGAAT 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  988 AATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTC 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      928 TCGGAATGAATTTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGT1CTCCTGC 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     868 CCAGTCAGCTGCCTCATTGGAGATTTCAACAATTGGGACGCAAATGCTGACATTATGAC 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         808 AAAAATGGGTTTCACTCGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTTGGTGC 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 aaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcaccaggagc 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748 ACTGAGGGAGGCAATTGACAAGTATGAGGGTGGTTTTGGAAGCCTTTTCTCGTGGTTATGA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 agatecaagettgacaggetttegteaacacetagattaceggtatteacagtacaaaag 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628 TGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAAGATT1ATGAAAT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 aattggatctaaaccaaggtccattcctccacccggcagagggcaaagaatatatgacat 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 TGGTAAACTGGAGGAGTCTAAAACATTAAATACTTCTGAAGAGACAATTATTGATGAATC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 tgttgaagatgaagtaaataaagaatctgttccaatgcgggagacagttagcetcagaaa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 tacgtgggctgcattgattggagatttcaataactggaatcctaatgcagatotcatgac 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   688 AGACCCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAG1 ACAAGAA 747
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                                                                                                                                               cacatatgccaactttagagatgatgtgcttcctcgcatcaaaaagcttggctacaatgc 1066
                                                                                                                                                                                                                                                                                                           aaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccagtaattaa 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                           atactatgatcctcccgaggaggaggaggtatgtgttcaaaaaatcctcagccaaagagacc 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aattccccatggttctcgagtaaagatacgcatggatactccatctggcaacaaagattc 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcagaatgagtgtggtgtctgggagatctttttgccgaataatgcagatggttcaccacc 766
                                                                                                                                                                                                                                                                                                                                                                                                               ACATTATGATCCACCCGAAGAGGAGGAGGTATATCTTCCAACACCCCACGGCCAAAGAAACC 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         actocgagaagaaattgacaagtatgaaggtagtotggatgcattttctcgtggctatga 586
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284. .2785
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AESHDQALVGGNTIAFWLMDKOMYDFMALDRSGTSLIDRGIŁLHKMIRLYTMGLGGEG
YLNFMGNEFGHPEWIDFPRAEQHLSDGSVIFGNQFSYDKCRFRFDLGDAEYLRYRGLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          con,R.A., Bewley,J.D., Smith,A.M., Bhattacharyya,M.K., Tatge,H. Ring,S., Bull,V., Hamilton,W.D. and Martin,C. Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development plant J. 7 (1), 3-15 (1995) 95201826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-JUL-1994) R.A. Burton, John Innes Institute, Colney Lane, Norwich NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabalees; Papilionoideae; Pisum.

1 (bases 1 to 3549)
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                      364. .2985
/gene="SBEI"
                                                                                                                                                                                                                                                                                                                             /gene=
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                                                                                                                                                                                                                                                                                                                                                                               EVESETTO
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SDDTLFGGFNRLNHTAEYFTSEGWYDDRPRSFLVYAPSRTAVYYALADGVESEPIELS
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                                                                                                                                                                                                 Score 1475.2;
Pred. No. 0;
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413;

0; Gaps

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577

517 782

DB 14; Length 3549; Indels

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1598 tgaagatgttagtggaatgccaacagtttgcattccggttgaagatggtggtggtggctt 1657
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                                                                          1803 TIACATGATGCTTGATGATCTCATTCACGGGCTCTTCCCTGAAGCTGTTTCAATIGG 1862
                                                                                                            1538 ttatttgatgctgttgaatgatatgattcatggtctctttcccagaggctgtcaccattgg 1597
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                                                                                                                                                                                                                                                                                                                                  tgatgggttcagatttgatggggtgacttcaatgatgtacaccccatcatggattgcaggt 1477
                                                                                                                                                                                                                                                                                                                                                                                                         CTGGGAAGTACTAAGGTACCTACTTTCAAATGCAAGATGGTGGCTGGATGAATATAAGTT 1682
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2763 TGAATCAGAGCCAATTGAACTGTCAGATGGAGTAGA 2798
                                                                                                                  2438 atcottcatggtgtacacaccatgtagaacagcagtggtctatgctttagtgg:ggatga 2497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2223 TGAAGGGTATTTGAATTTTATGGGGAATGAATTCGGACATCCTGAGTGGATCG&TTTTCC 2282
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                                       2498 agtggagaatgaattggaacctgtcgccggttaaga 2533
                                                                                       2703 ATCTTTCCTCGTTTATGCACCTTCTAGAACAGCAGTGGTGTATGCCCCTTGCGGATGGAGT 2762
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                                                                                                                                                                              2643 TAGGCTCAATCATACTGCTGAGTACTTCACCTCTGAAGGGTGGTATGATGACCGGCCTCG
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LOCUS
DEFINITION
ACCESSION KEYWORDS SOURCE RESULT AB029548 VERSION ORGANISM AB029548

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Phaseolus AB029548 3360 bp mRNA PLN 1()-JUL-1999 algaris kbel mRNA for branching enzyme 1, complete

branching enzyme 1.
Phaseolus vulgaris cDNA &
Phaseolus vulgaris AB029548.1 GI:5441245 mRNA.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;

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1561 TCACCCAGAGTGGATTGATTTCCCTAGAGGTGAACAACGCCTTCCTGATGGTTCAGTTCT 1620
                   1994 acaccccgagtggattgattttccaagaggtgatctacatcttcccagtggtaaatttgt 2053
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                                                                       ACTTATAACTATGGGATTAGGAGGAGGAAGGATATCTAAATTTCÄTGGGGAACGAATTTGG
                                                                                              gcttattaccatgggattaggcggagaaggatattttgattttjatgggaaatgaatttgg 1993
                                                                                                                                                                     tettgacagaceatetaeteeteteatagategtggagtågeattgcacaaaatgateag 1933
                                                                                                                                                                                                                                                                                                                                   gaccaacaggcggtggttggaaaagtgtgtttcttatgctgaaagtcatgaccaggccct 1813
                                                                                                                                                  TCTGGATAGACCAGCAACGCCAGTAATAGACCGTGGAATAGKATTGCATAAAATGATCAG
                                                                                                                                                                                                                               TGTTGGTGATAAAACTATAGCGTTCTGGTTGATGGACA
                                                                                                                                                                                                                                                  tgttggtgacaaaactattgcattttggctgatggachaggatatgtatgacttcatggc
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                                                                                                                                                                                                                                                                                                                                                                                 GATTGAGATTCTCAAGAGAAGAGATGAGGATTGG
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                                                                                                                                                                                                                                                                                                Submitted (09-MAR-1995) Dane K. Fisher, Horticulture, State University. 103 Tyson Bldg., University Park, P. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              Fisher, D.K., Gao, M., Kim, K.-N., Boyer, C.D. and Guiltinan, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 2542)
Fisher,D.K., Gao,M., Kim,K.N., Boyer,C.D. and Guiltinan,M.J.
Two closely related cDNAs encoding starch branching enzyme from
Arabidopsis thaliana
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/codon_start=1
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6-alpha-d-(1,4-alpha-d-glucano)-transferase"
/product="starch branching enzyme class II"
/protein_id="AAB03100.1"
                                                                                                     /gene="sbe2-2"
/EC_number="2.4.1.18"
                                                                                                                                                                    /gene="sbe2-2"
                                                                                                                                                                                           /tissue_type="hypocotyl"
1. .2403
                                                                                                                                                                                                                          /strain="ecotype Columbia"
/db_xref="taxon:3702"
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Query Match 47.8%; Score 1392.4; DB 14; Length 2542; Best Local Similarity 79.0%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 441; Indels 0; 1120 acgtcacaaacttttatýcagctagcagccgatttggaactcctgatgatttaaagtctc 1179 460 atgacatagatccaagcttgacaggctttcgtcaacacctagattaccggtattcacagt 519 362 ATGAGATAGACCCCATGTTACGAACTTACAACAATCATCTTGATTACCGTTATGGACAGT 421 602 TCATGACTCGGAATGAATTTGGTGTTTTGGGAGATCTTTTTGCCCCAACAACACTGATGGTT 661 482 GCTATGAAAAGTTAGGATTTTCGCGCAGTGATGCCGGTATAACTTATAGAGAGTGGGCGC 541 580 gctatgaaaagtttggtttctcacgcagtgaaacaggaataacttatagagagtgggcac 639 520 acamaagactccgagaagaaattgacaagtatgaaggtagtctggatgcattttctcgtg 579 842 AGAGACCTAAGTCGCTAAGGATTTATGAAGCACATGTTGGCATGAGTAGCACGGAACCAA 901 820 aagattotattootgottggatcaagttotoagttoaagcaccaggtgaactoccatata 879 700 tcatgactcagaatgagtgtgtgtctgggagatctttttgccgaataatgcagatggtt 759 962 ATAATGCTGTTCAAATTATGGCCATACAAGAACATTCATATTATGCCAGCTTTGGGTACC 1021 940 agagaccaaaatcacttcggatttatgagtcgcacgttggaatgagtagtacggagccag 999 880 atggcatatactatgatcctcccqaggaggaggagtatgtgttcaaaaatcctcagccaa 939 722 AAGACTCAATTCCTGGATCAAGTTCTCGGTGCAAGCTCCAGGTGAAATCCCATTCA 781 743 a 499 c 579 g 721 t 0; Gaps ۵. 0,

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92	attgattttcca ATTGATTTTCCC	
6 0	Qy 1900 tagatcgtggagtagcattgcacaaaatgatcaggcttattaccatgggattaggaggag 	_ ^
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44.	Qy 1480 attttaccggcaactacaatgaatactttggatatgcaactgatgtagatgctgi:ggttt 1	g Ø
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ω 4-	360 gggaggttotaaggtttottotttcaaatgcaaggtggttggttggatgagtacazgtttg 1 	<u>p</u> 0
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239 141	OY 1180 taatagataaagotcaogagttaggtcttcttgttctcatggatattgttcatagccatg 1 	B 8
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larsson,C.T., Khoshnoodi,J., Ek,B., Rask,L. and Larsson,H. Molecular cloning and characterization of starch-branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnoliophyta; eudicotyledons; core eudicots; I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larsson, C.T.A.
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                                        */translation="ekssynsesrpstvaasgkvlvpgtqsdssssstdofeefretspenspastdvdsstmehasglikespenspastdvdsstmehasglikespenspastdvdsstmehasglikespenspastdvsstmeldpassgvkklera dlytseetiildesdrikergippglikespenspastdyrklera dkyrgglebasrsryermgftrsatgityremapgaqsaaligdenmadanadimyrne grybeifyrnstydberyrikespyngtyrdbelpprestynglyrikespepklikespyngtyrdbelpprestynglyrikespepklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenklikespenkli
ASNNTLDGLNMFDGTDSCYFHSGARGYHWMWDSRLFNYGNWEVLRYLLSNARWWLDEF
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/db_xref="GI:2764396"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="starch branching enzyme II, SBE-II"
                                                                                                                                                                                                                                                                                                                                                       /db_xref-"SPTREMBL:049953"
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/plasmid="pALSBE-II (#123)"
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/function="branches 1,4-alpha glucans"
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/EC_number="2.
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1187 taaaagctcacgagttaggtcttcttgttctcatggatattgttcatagccatgcatcaac 1246
                                                      1007
                                                                                                     1127 aaacttttatgcagctagcagccgatttggaactcctgatgatttaaagtctctaataga 1186
                                                                                                                                                                                       1067 tgttcagctcatggctattcaagagcattcatattatgctagttttgggtatcacgtcac 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           825 ATATTATGATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCCACGGCCAAAGAAACC
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                                                                                                                                                                                                                                                                                                  cacatatyccaactttagagatyatytycttcctcycatcaaaaaycttyyctacaatyc 1066
                                                                                                                                                                                                                                                                 CTCATACGTGAATTTTAGAGATGAAGTTCTTCCTCGCATAAAAAAGCTTGGGTACAATGC
                                                                                                                                                                                                                                                                                                                                                                      AAAGT¢G¢tgagaatatatgaat¢tcatattggaatgagtagt¢cggag¢¢taaaattaa
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LVTMGLGGEGYLNFMGNEFGHPEWIDFPRAEQHLSDGSVIPGNQFSYDKCRRRFDLGD
AEYLAYRGLQEFDRAMQYLEDKYEFMTSEHQFISRKDEGDRMIVFEKGNLVFVFNFHW
TKSYSDYRIGCLKPGKYKVALDSDDPLFGGFGRIDHNAEYFTFEGWYDDRPRSIMVYA
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76.8%;
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Pred. No. 0;
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